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OM protein - protein search, using sw model

Run on: May 11, 2004, 16:20:26 ; Search time 23 Seconds
(without alignments)
693.584 Million cell updates/sec

Title: US-09-827-271-392

Perfect score: 1574
Sequence: 1 HASAHASGRORQLHSASTQI.....SSFAISWALLPISPYLMK 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Match	Length	ID	Description
1	1574	100.0	309	US-09-404-879A-392	Sequence 392, App *
2	1431	90.9	282	US-09-404-879A-393	Sequence 393, App *
3	247	15.7	316	US-09-910-174B-24	Sequence 24, App1
4	247	15.7	316	US-09-620-461-24	Sequence 24, App1
5	246	15.6	441	US-09-651-200-4	Sequence 4, App1
6	246	15.6	534	US-09-651-200-6	Sequence 6, App1
7	246	15.6	534	US-09-651-200-24	Sequence 24, App1
8	245	15.6	340	US-09-651-200-2	Sequence 2, App1
9	238.5	15.2	315	US-09-910-174B-28	Sequence 28, App1
10	238.5	15.2	315	US-09-620-461-28	Sequence 28, App1
11	223	14.2	513	US-09-910-174B-18	Sequence 18, App1
12	223	14.2	513	US-09-620-461-18	Sequence 18, App1
13	217.5	13.8	540	US-08-724-394A-4	Sequence 4, App1
14	215.5	13.7	731	US-09-910-174B-15	Sequence 15, App1
15	215.5	13.7	731	US-09-620-461-15	Sequence 15, App1
16	213.5	13.6	584	US-09-910-174B-16	Sequence 16, App1
17	213.5	13.6	584	US-09-620-461-16	Sequence 16, App1
18	212.5	13.5	610	US-08-724-394A-5	Sequence 5, App1
19	211.5	13.4	526	US-09-910-174B-9	Sequence 9, App1
20	211.5	13.4	526	US-09-620-461-9	Sequence 9, App1
21	211.5	13.4	589	US-08-724-394A-1	Sequence 1, App1
22	207.5	13.2	319	US-09-910-174B-12	Sequence 12, App1
23	207.5	13.2	319	US-09-620-461-12	Sequence 12, App1
24	207.5	13.2	342	US-08-724-394A-6	Sequence 6, App1
25	207.5	13.2	357	US-09-910-174B-14	Sequence 14, App1
26	207.5	13.2	357	US-09-620-461-14	Sequence 14, App1
27	204	13.0	290	US-09-910-174B-19	Sequence 19, App1

28	204	13.0	290	4	US-09-620-461-19	Sequence 19, App1
29	204	13.0	350	4	US-09-651-200-25	Sequence 25, App1
30	204	13.0	350	4	US-09-910-174B-17	Sequence 17, App1
31	204	13.0	350	4	US-09-620-461-17	Sequence 17, App1
32	199.5	12.7	290	4	US-09-910-174B-32	Sequence 32, App1
33	196	12.5	296	4	US-09-667-135-36	Sequence 36, App1
34	193	12.3	527	4	US-09-910-174B-10	Sequence 10, App1
35	193	12.3	527	4	US-09-620-461-10	Sequence 10, App1
36	192	12.2	329	4	US-09-651-200-18	Sequence 18, App1
37	192	12.2	329	4	US-09-303-040-6	Sequence 6, App1
38	188.5	12.0	290	4	US-09-910-174B-8	Sequence 8, App1
39	188.5	12.0	290	4	US-09-620-461-8	Sequence 8, App1
40	186	11.8	529	4	US-09-910-174B-13	Sequence 13, App1
41	186	11.8	529	4	US-09-620-461-13	Sequence 13, App1
42	186	11.8	523	2	US-08-724-394A-2	Sequence 2, App1
43	183	11.6	523	2	US-09-910-174B-11	Sequence 11, App1
44	183	11.6	523	2	US-09-620-461-11	Sequence 11, App1
45	183	11.6	581	2	US-08-724-394A-3	Sequence 3, App1

ALIGNMENTS

RESULT 1	US-09-404-879A-392	Sequence 392, Application US/09404879A
Patent No. 6468546		
GENERAL INFORMATION:		
APPLICANT: Mitcham, Jennifer L.		
APPLICANT: King, Gordon E.		
APPLICANT: Algate, Paul A.		
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND		
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER		
FILE REFERENCE: 210121.462C2		
CURRENT FILING DATE: US/09/404, 879A		
CURRENT FILING DATE: 1999-09-24		
NUMBER OF SEQ ID NOS: 393		
SOFTWARE: FastSeq for Windows Version 3.0		
SEQ ID NO 392		
LENGTH: 309		
TYPE: PRT		
ORGANISM: Homo sapiens		
US-09-404-879A-392		
Query Match	100.0%;	Score 1574; DB 4; Length 309;
Best Local Similarity	100.0%;	Pred. No. 1.3e-153; Indels 0; Gaps 0;
Matches	309;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	HASAHASGRORQLHSASTQIRWEPSPAMASIGQLFMSIIIIIIAGAMLIIGFISG 60
DB	1	HASAHASGRORQLHSASTQIRWEPSPAMASIGQLFMSIIIIIIAGAMLIIGFISG 60
QY	61	RHSITVTIVASAGNIGEDGIIISCTFEPIKISDIYIOWLKRGVGLVHFFRGKELSEQ 120
DB	61	RHSITVTIVASAGNIGEDGIIISCTFEPIKISDIYIOWLKRGVGLVHFFRGKELSEQ 120
QY	121	DEMRGRTRAVADQYIVGNASIRLKNVQITAGTYKCYIIISKGGNNLEKKTGAFSMP 180
DB	121	DEMRGRTRAVADQYIVGNASIRLKNVQITAGTYKCYIIISKGGNNLEKKTGAFSMP 180
QY	181	EVNDVYNASSETLRCEAPRMPPOPTVVASGVQDQANFSEVNTSFEINSEVTKVYSV 240
DB	181	EVNDVYNASSETLRCEAPRMPPOPTVVASGVQDQANFSEVNTSFEINSEVTKVYSV 240
QY	241	LYNVTINNTYSCMIENDIAKATGDIKTESSEIKRSHQOLNSKSKSLCVSSFFAISWALL 300
DB	241	LYNVTINNTYSCMIENDIAKATGDIKTESSEIKRSHQOLNSKSKSLCVSSFFAISWALL 300
QY	301	PLSPYLMK 309
DB	301	PLSPYLMK 309

RESULT 2
 US-09-404-879A-393
 ; Sequence 393, Application US/09404879A
 ; Patent No. 6468546
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: King, Gordon E.
 ; APPLICANT: Algate, Paul A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.462C2
 ; CURRENT APPLICATION NUMBER: US/09/404, 879A
 ; CURRENT FILING DATE: 1999-09-24
 ; NUMBER OF SEQ ID NOS: 393
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 393
 ; LENGTH: 282
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-404-879A-393

Query Match 90.9%; Score 1431; DB 4; Length 282;
 Best Local Similarity 100.0%; Pred. No. 5,8e-139;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASIGQLPMSIIIIIIIIAGATATLIGFISGRHSITVTTVASAGNIGEDGILSTFEP 87
 DB 1 MASIGQLPMSIIIIIIIIAGATATLIGFISGRHSITVTTVASAGNIGEDGILSTFEP 60
 QY 88 DIKLSDIVIOMKEGVLGVHFEKKGDELSEODEMFRGRTAVFADQVIVGNASLRLKNV 147
 DB 61 DILSDIVIOMKEGVLGVHFEKKGDELSEODEMFRGRTAVFADQVIVGNASLRLKNV 120
 QY 148 QLTDACTYKCYITTSKGGKMANLEYKTGAFSMEPVNDVNASSETLRCEAPRPFQPTV 207
 DB 121 QLTDACTYKCYITTSKGGKMANLEYKTGAFSMEPVNDVNASSETLRCEAPRPFQPTV 180
 QY 208 MASOVDOGAFSEVNTSFEINSENVTKVSVLYNVNTINNTSCMIENDIAKATGDIKY 267
 DB 181 MASOVDOGAFSEVNTSFEINSENVTKVSVLYNVNTINNTSCMIENDIAKATGDIKY 240
 QY 268 TSEIKRRSHLOLINSKASLCVSSFPALISWALLPLSPYMLX 309
 DB 241 TSEIKRRSHLOLINSKASLCVSSFPALISWALLPLSPYMLX 282

RESULT 3
 US-09-910-174B-24
 ; Sequence 24, Application US/09910174B
 ; Patent No. 6630575
 ; GENERAL INFORMATION:
 ; APPLICANT: Coyle, Anthony J.
 ; APPLICANT: Fraser, Christopher C.
 ; APPLICANT: Manning, Stephen
 ; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
 ; TITLE OF INVENTION: Family and Uses Thereof
 ; FILE REFERENCE: 35800/236924
 ; CURRENT APPLICATION NUMBER: US/09/910, 174B
 ; CURRENT FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: US 09/620,461
 ; PRIORITY FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24
 ; LENGTH: 316
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-910-174B-24

Query Match 15.7%; Score 247; DB 4; Length 316;
 Best Local Similarity 28.5%; Pred. No. 5.3e-17;
 Matches 74; Conservative 46; Mismatches 106; Indels 34; Gaps 10;

QY 20 IRMEPSPAMASIGQLPMSIIIIIIAGATATLIGFISGRHSITVTTVASAGNIGEDG 79
 DB 2 LRRRGSPGNG-----VHVGAALGALMFCLTGALVQVPEDPVALVGTDA 46
 QY 80 ILSCF--EPDIKLSDIVIOMKEGVLGVHFEKKGDELSEODEMFRGRTAVFADQVIV 137
 DB 47 TLCCSFSPGPGSLAQNLINQLTDTKQLVHSPABQD---QGSAYANRTALFEDLLAQ 102
 QY 138 GNASIRLKNVQLTDAGTYKCYITTSKGGKMANLEYKTGA-FSMEPVNDVY----ASSE 191
 DB 103 GNASIRLQVRVADGESFTCF-VSIRDFGSAVSLQVAPYKSPMTLEPNKDLRPGDTV 161
 QY 192 TLRCAPRPFQPTVVMASOVDOGAFSEVNTSFEINSENVTKVSVLYNVNT-INTY 250
 DB 162 TITCSYRGYPAEVFW--QDGQGVPLTGNVTT-QMANGQLFDVHSLRVVLGANGTY 218
 QY 251 SCMIENDIAK--ATGDIKYT 268
 DB 219 SCLVRNPVLQODAHGSVTIT 238

RESULT 4
 US-09-620-461-24
 ; Sequence 24, Application US/09620461
 ; Patent No. 6635750
 ; GENERAL INFORMATION:
 ; APPLICANT: Coyle, Anthony J.
 ; APPLICANT: Fraser, Christopher C.
 ; APPLICANT: Manning, Stephen
 ; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
 ; TITLE OF INVENTION: Family and Uses Thereof
 ; FILE REFERENCE: 5800-149
 ; CURRENT APPLICATION NUMBER: US/09/620,461
 ; CURRENT FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 24
 ; LENGTH: 316
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-620-461-24

Query Match 15.7%; Score 247; DB 4; Length 316;
 Best Local Similarity 28.5%; Pred. No. 5.3e-17;
 Matches 74; Conservative 46; Mismatches 106; Indels 34; Gaps 10;

QY 20 IRMEPSPAMASIGQLPMSIIIIIIAGATATLIGFISGRHSITVTTVASAGNIGEDG 79
 DB 2 LRRRGSPGNG-----VHVGAALGALMFCLTGALVQVPEDPVALVGTDA 46
 QY 80 ILSCF--EPDIKLSDIVIOMKEGVLGVHFEKKGDELSEODEMFRGRTAVFADQVIV 137
 DB 47 TLCCSFSPGPGSLAQNLINQLTDTKQLVHSPABQD---QGSAYANRTALFEDLLAQ 102
 QY 138 GNASIRLKNVQLTDAGTYKCYITTSKGGKMANLEYKTGA-FSMEPVNDVY----ASSE 191
 DB 103 GNASIRLQVRVADGESFTCF-VSIRDFGSAVSLQVAPYKSPMTLEPNKDLRPGDTV 161
 QY 192 TLRCAPRPFQPTVVMASOVDOGAFSEVNTSFEINSENVTKVSVLYNVNT-INTY 250
 DB 162 TITCSYRGYPAEVFW--QDGQGVPLTGNVTT-QMANGQLFDVHSLRVVLGANGTY 218
 QY 251 SCMIENDIAK--ATGDIKYT 268
 DB 219 SCLVRNPVLQODAHGSVTIT 238

RESULT 5
 US-09-651-200-4
 ; Sequence 4, Application US/09651200
 ; Patent No. 6429303
 ; GENERAL INFORMATION:
 ; APPLICANT: Green et al

DR N-PSDB; AA265059.
 XX Membrane-bound proteins and related nucleotide sequences.
 XX
 XX
 PS Claim 12; Fig 208; 822pp; English.
 XX
 CC The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIR
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
 CC also be useful for the preparation of PRO polypeptides, especially by
 CC recombinant techniques
 CC
 XX Sequence 282 AA;
 SQ

WCA943088-A2

Query Match 90.9%; Score 1431; DB 3; Length 282;
 Best Local Similarity 100.0%; Pred. No. 2.2e-117;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGGILFMSIIISIIIIAGAILIIGFISGRHSITVTVAASAGNIGEDGILSTFEP 87
 DB 1 MASLGGILFMSIIISIIIIAGAILIIGFISGRHSITVTVAASAGNIGEDGILSTFEP 60
 QY 88 DIKLSDIVIOMLKEGVLGIVHEFEKQDELSEODEMFRGRTAVFADQVIVGNASRLKNV 147
 DB 61 DIKLSDIVIOMLKEGVLGIVHEFEKQDELSEODEMFRGRTAVFADQVIVGNASRLKNV 120
 QY 148 QLTDACTYKCYIITTSKGNANILEYKTGAFSPMEVNVVDYNASSETLRCAAPRMFPPTVV 207
 DB 121 QLTDACTYKCYIITTSKGNANILEYKTGAFSPMEVNVVDYNASSETLRCAAPRMFPPTVV 180
 QY 208 MASQVDOGANFSEVNTSEFELNSENVTMKVSVLYNVTTNTNTYSCMIENDIAKATGDIKY 267
 DB 181 MASQVDOGANFSEVNTSEFELNSENVTMKVSVLYNVTTNTNTYSCMIENDIAKATGDIKY 240
 QY 268 TSEIKRRSHLOLNSKASLCVSSFPFATSWALLPLSPYIMLK 309
 DB 241 TSEIKRRSHLOLNSKASLCVSSFPFATSWALLPLSPYIMLK 282

RESULT 6
 AAB12557
 ID AAB12557 *standard; protein; 282 AA.
 XX
 AC AAB12557;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Human ovarian carcinoma antigen OBE protein SEQ ID NO:393.
 XX
 KM Human: ovarian carcinoma; ovarian cancer; therapy; diagnosis;
 KM tumour antigen; identification; cytostatic; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200036107-A2.
 XX
 PD 22-JUN-2000.
 XX
 PF 17-DEC-1999; 99WO-US030270.
 XX
 PR 17-DEC-1998; 98US-00215681.
 PR 17-DEC-1998; 98US-00216003.
 PR 23-JUN-1999; 99US-00338933.
 PR 24-SEP-1999; 99US-00404879.

XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Mitcham JI, King GE, Algate PA, Frudakis TN;
 XX
 DR WPI; 2000-431589/37.
 XX
 PS Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
 PS encoding it, useful for the diagnosis, prevention and treatment of
 PT cancer, preferably ovarian cancer.
 XX
 XX Example 2; Page 207; 299pp; English.
 XX
 CC The present invention describes an isolated polypeptide comprising an
 CC immunogenic portion of an ovarian carcinoma protein (or its variants).
 CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
 CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian
 CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
 CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
 CC cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human
 CC ovarian carcinoma polynucleotides and proteins used in the
 CC exemplification of the present invention
 CC
 XX Sequence 282 AA;
 SQ

Query Match 90.9%; Score 1431; DB 3; Length 282;
 Best Local Similarity 100.0%; Pred. No. 2.2e-117;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGGILFMSIIISIIIIAGAILIIGFISGRHSITVTVAASAGNIGEDGILSTFEP 87
 DB 1 MASLGGILFMSIIISIIIIAGAILIIGFISGRHSITVTVAASAGNIGEDGILSTFEP 60
 QY 88 DIKLSDIVIOMLKEGVLGIVHEFEKQDELSEODEMFRGRTAVFADQVIVGNASRLKNV 147
 DB 61 DIKLSDIVIOMLKEGVLGIVHEFEKQDELSEODEMFRGRTAVFADQVIVGNASRLKNV 120
 QY 148 QLTDACTYKCYIITTSKGNANILEYKTGAFSPMEVNVVDYNASSETLRCAAPRMFPPTVV 207
 DB 121 QLTDACTYKCYIITTSKGNANILEYKTGAFSPMEVNVVDYNASSETLRCAAPRMFPPTVV 180
 QY 208 MASQVDOGANFSEVNTSEFELNSENVTMKVSVLYNVTTNTNTYSCMIENDIAKATGDIKY 267
 DB 181 MASQVDOGANFSEVNTSEFELNSENVTMKVSVLYNVTTNTNTYSCMIENDIAKATGDIKY 240
 QY 268 TSEIKRRSHLOLNSKASLCVSSFPFATSWALLPLSPYIMLK 309
 DB 241 TSEIKRRSHLOLNSKASLCVSSFPFATSWALLPLSPYIMLK 282

RESULT 7
 AAU29132
 ID AAU29132 standard; protein; 282 AA.
 XX
 AC AAU29132;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human PRO polypeptide sequence #109.
 XX
 KM PRO polypeptide; mammary tumour; cancer; human; cattle; horse; sheep;
 KM dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KM blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KM adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200168848-A2.
 XX
 PD 20-SEP-2001.
 XX
 PR 28-FEB-2001; 2001WO-US006520.

01-MAR-2000; 2000MO-US005601.
 PR 02-MAR-2000; 2000MO-US005841.
 PR 03-MAR-2000; 2000MO-US005841.
 PR 06-MAR-2000; 2000US-0186968P.
 PR 14-MAR-2000; 2000US-0189320P.
 PR 14-MAR-2000; 2000US-0189328P.
 PR 15-MAR-2000; 2000MO-US006884.
 PR 21-MAR-2000; 2000US-0190828P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000US-0191048P.
 PR 21-MAR-2000; 2000US-0191314P.
 PR 28-MAR-2000; 2000US-0192655P.
 PR 29-MAR-2000; 2000US-0193032P.
 PR 29-MAR-2000; 2000US-0193053P.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 04-APR-2000; 2000US-0194449P.
 PR 04-APR-2000; 2000US-0194647P.
 PR 11-APR-2000; 2000US-0195975P.
 PR 11-APR-2000; 2000US-0196000P.
 PR 11-APR-2000; 2000US-0196187P.
 PR 11-APR-2000; 2000US-0196690P.
 PR 11-APR-2000; 2000US-0196820P.
 PR 18-APR-2000; 2000US-0198121P.
 PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000MO-US013705.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000MO-US020710.
 PR 22-AUG-2000; 2000US-0064848.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 20-DEC-2000; 2000MO-US034956.
 XX
 PA (GENTH) GENENTECH INC.
 XX Baker KP, Chen J, Desnucers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX N-PSDB; AAS46033.
 DR WPI: 2001-602746/68.
 XX
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX
 PS Claim 11; Fig 218; 774pp; English.
 XX
 CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumor in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumor in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumor necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumors and also
 CC susceptibility to tumor development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumors, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX
 SQ Sequence 282 AA.

Query Match 90.9%; Score 1431; DB 4; Length 282;
 Best Local Similarity 100.0%; Pred. No. 2.2e-117;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 28 MASIGQILFWISIIIIIIIIAGALIIIGFGISGRHSITVTVASAGNIGEDGIIISCTEP 87
 DB 1 MASIGQILFWISIIIIIIIIAGALIIIGFGISGRHSITVTVASAGNIGEDGIIISCTEP 60
 QY 88 DIKSDIYIOWLKEGVGLVHEFEKGEKDELSEQDMFGRGTAVFADQYIVGNASIRLKNV 147
 DB 61 DIKSDIYIOWLKEGVGLVHEFEKGEKDELSEQDMFGRGTAVFADQYIVGNASIRLKNV 120
 QY 148 QLTDAQTKCYITISKGNANLVEYKTGAFSMEPVNVVYNASSETLRCEAPRPFOPPTV 207
 DB 121 QLTDAQTKCYITISKGNANLVEYKTGAFSMEPVNVVYNASSETLRCEAPRPFOPPTV 180
 QY 208 WASQVDQGANFSEVSNFSFELNSENVTMKVSVLYNVITINNTYSCMIENDIAKATGDIKY 267
 DB 181 WASQVDQGANFSEVSNFSFELNSENVTMKVSVLYNVITINNTYSCMIENDIAKATGDIKY 240
 QY 268 TSEETKRSHQLQLNSKASLGVSSFFAISWALLPSPYIMLK 309
 DB 241 TSEETKRSHQLQLNSKASLGVSSFFAISWALLPSPYIMLK 282
 RESULT 8
 AAB87555 standard; protein; 282 AA.
 XX
 AC AAB87555;
 XX
 DT 15-MAY-2001 (first entry)
 XX
 DE Human PRO1291.
 XX
 KW Human; PRO protein; mapping.
 XX
 OS Homo sapiens.
 XX
 PN WO200116318-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 24-AUG-2000; 2000MO-US023328.
 XX
 PR 01-SEP-1999; 99MO-US020111.
 PR 15-SEP-1999; 99MO-US021090.
 PR 07-DEC-1999; 99US-0169495P.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 18-FEB-2000; 2000MO-US004342.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 01-MAR-2000; 2000MO-US005601.
 PR 21-MAR-2000; 2000US-0187202P.
 PR 30-MAR-2000; 2000US-0191007P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 05-JUN-2000; 2000US-0209832P.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Eaton DL, Filvaroff E, Gerlitsen ME, Goddard A, Godowski PJ;
 XX Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
 XX WPI: 2001-183260/18.
 DR N-PSDB; AAF92087.
 XX
 PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
 PT biology, including use as hybridization probes, and in chromosome and
 PT gene mapping.
 XX

SQ Sequence 309 AA:

Query Match 100.0%; Score 1574; DB 3; Length 309;
 Best Local Similarity 100.0%; Pred. No. 6,7e-130;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAASGROROLHASTQIRWEPSPAMASLGQILFWSIIISIIIIILAGAILIIGFGISG 60
 DB 1 HASAASGROROLHASTQIRWEPSPAMASLGQILFWSIIISIIIIILAGAILIIGFGISG 60
 QY 61 RHSITVTVASAGNIGEDGILSCTFEEDIKLSDIVIQWLKEGVGLVHFEKGDSEQ 120
 DB 61 RHSITVTVASAGNIGEDGILSCTFEEDIKLSDIVIQWLKEGVGLVHFEKGDSEQ 120
 QY 121 DEMFGRTAFAVDQYIVGNASRLKNVQLTDAGTYKCIITTSKGGKGNANLEYKTGAFSMP 180
 DB 121 DEMFGRTAFAVDQYIVGNASRLKNVQLTDAGTYKCIITTSKGGKGNANLEYKTGAFSMP 180
 QY 181 EVNDYNASSETLRCEAPRPFQPTVVMASQVDGANSFSEVSNFSFELNSENVTMKVSV 240
 DB 181 EVNDYNASSETLRCEAPRPFQPTVVMASQVDGANSFSEVSNFSFELNSENVTMKVSV 240
 QY 241 LYNVTINNYSQMIENDIAKATGDIKVTESIKRSHQLINSKASLCVSSFFAISWALL 300
 DB 241 LYNVTINNYSQMIENDIAKATGDIKVTESIKRSHQLINSKASLCVSSFFAISWALL 300
 QY 301 PLSPYLMK 309
 DB 301 PLSPYLMK 309

RESULT 2

AAB99205
 ID AAB99205 standard; protein; 309 AA.

AAB99205;

04-SEP-2001 (first entry)

Human ovarian tumour-derived antigen OBE #2.

KM Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour;
 antigen; OBE.

OS Homo sapiens.

PN WO200140269-A2.

PD 07-JUN-2001.

PF 29-NOV-2000; 2000WO-US032520.

PR 30-NOV-1999; 99US-00451651.

PR 22-FEB-2000; 2000US-00510662.

PR 10-MAR-2000; 2000US-00523586.

PR 07-APR-2000; 2000US-00545068.

PR 15-MAY-2000; 2000US-00571025.

PA (CORI-) CORIXA CORP.

PI Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;
 DR N-PSDB; AAH55681.

PT Breast tumor polypeptides and the nucleic acids that encode them, useful
 for the prevention, diagnosis and treatment of breast cancer.

PS Example 3; Page 191-192; 221pp; English.

CC The present invention relates to human breast tumour protein coding
 sequences (see AAH55479-AAH55513, AAH55517-AAH55679 and AAH55682-
 CC AAH55762). The breast tumour protein DNA sequences may be used in the

CC prevention, diagnosis and treatment of diseases associated with

CC inappropriate expression of the breast tumour protein e.g. breast cancer.

CC The present sequence is a human ovarian tumour-derived antigen, which was
 used in an example from the present invention

SQ Sequence 309 AA:

Query Match 100.0%; Score 1574; DB 4; Length 309;
 Best Local Similarity 100.0%; Pred. No. 6,7e-130;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAASGROROLHASTQIRWEPSPAMASLGQILFWSIIISIIIIILAGAILIIGFGISG 60
 DB 1 HASAASGROROLHASTQIRWEPSPAMASLGQILFWSIIISIIIIILAGAILIIGFGISG 60
 QY 61 RHSITVTVASAGNIGEDGILSCTFEEDIKLSDIVIQWLKEGVGLVHFEKGDSEQ 120
 DB 61 RHSITVTVASAGNIGEDGILSCTFEEDIKLSDIVIQWLKEGVGLVHFEKGDSEQ 120
 QY 121 DEMFGRTAFAVDQYIVGNASRLKNVQLTDAGTYKCIITTSKGGKGNANLEYKTGAFSMP 180
 DB 121 DEMFGRTAFAVDQYIVGNASRLKNVQLTDAGTYKCIITTSKGGKGNANLEYKTGAFSMP 180
 QY 181 EVNDYNASSETLRCEAPRPFQPTVVMASQVDGANSFSEVSNFSFELNSENVTMKVSV 240
 DB 181 EVNDYNASSETLRCEAPRPFQPTVVMASQVDGANSFSEVSNFSFELNSENVTMKVSV 240
 QY 241 LYNVTINNYSQMIENDIAKATGDIKVTESIKRSHQLINSKASLCVSSFFAISWALL 300
 DB 241 LYNVTINNYSQMIENDIAKATGDIKVTESIKRSHQLINSKASLCVSSFFAISWALL 300
 QY 301 PLSPYLMK 309
 DB 301 PLSPYLMK 309

RESULT 3

ABP30900
 ID ABP30900 standard; protein; 309 AA.

ABP30900;

02-JUL-2002 (first entry)

OBE protein #1.

KM Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.

OS Homo sapiens.

PN WO200206317-A2.

PD 24-JAN-2002.

PF 17-JUL-2001; 2001WO-US022635.

PR 17-JUL-2000; 2000US-00617747.

PR 10-AUG-2000; 2000US-00636801.

PR 20-SEP-2000; 2000US-00667857.

PR 04-APR-2001; 2001US-00827271.

PR 18-JUN-2001; 2001US-00884441.

PA (CORI-) CORIXA CORP.

PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
 DR Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
 DR N-PSDB; ABN72971.

PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma
 protein or its variant, useful for stimulating an immune response in a
 patient and treating ovarian cancer.

GenCore version 5.1.6
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OM protein - protein search, using 'sw model'

Run on: May 11, 2004, 16:00:15 ; Search time 59 Seconds
(without alignments) 1479.783 Million cell updates/sec

Title: US-09-827-271-392
Perfect score: 1574
Sequence: 1 HASAHASGRQRQLHNASSTQI.....SSFAISWALLPLESYMLK 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A.Geneseq_29Jan04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1574	100.0	309	3	AAH12556 Human ova
2	1574	100.0	309	4	AAH99205 Human ova
3	1574	100.0	309	5	ABP30900 OBE prote
4	1574	100.0	309	7	ADA08545 Human ova
5	1431	90.9	282	3	AAH66719 Membrane
6	1431	90.9	282	3	AAH12557 Human ova
7	1431	90.9	282	4	AAU29132 Human PRO
8	1431	90.9	282	4	AAH87555 Human PRO
9	1431	90.9	282	4	AAH99204 Human ova
10	1431	90.9	282	4	AAH65242 Human PRO
11	1431	90.9	282	5	AAE20311 Human B7-
12	1431	90.9	282	5	ABG96445 Human ova
13	1431	90.9	282	5	AAU77766 Tumour as
14	1431	90.9	282	5	ABG95880 Human sec
15	1431	90.9	282	5	AAU77766 Tumour as
16	1431	90.9	282	5	ABP30901 OBE prote
17	1431	90.9	282	5	ABH76274 Breast BS
18	1431	90.9	282	5	AAH18336 Human B7-
19	1431	90.9	282	5	ABH09879 Amino aci
20	1431	90.9	282	5	AAH19013 Human B7-
21	1431	90.9	282	6	ABU58508 Human PRO
22	1431	90.9	282	6	ABU88056 Novel hum
23	1431	90.9	282	6	ABU84371 Human sec
24	1431	90.9	282	6	ABH66245 Human sec
25	1431	90.9	282	6	ABH65635 Human sec

26	1431	90.9	282	6	ABU99575 Human sec
27	1431	90.9	282	6	ABU58057 Human PRO
28	1431	90.9	282	6	ABU59135 Novel hum
29	1431	90.9	282	6	ABU82647 Human sec
30	1431	90.9	282	6	ABU82814 Human PRO
31	1431	90.9	282	6	ABU89935 Novel hum
32	1431	90.9	282	6	ABH68184 Human sec
33	1431	90.9	282	6	ABU60566 Human sec
34	1431	90.9	282	6	ABU96237 Novel hum
35	1431	90.9	282	6	ABU92668 Human sec
36	1431	90.9	282	6	ABO08745 Human sec
37	1431	90.9	282	6	ABO02797 Human sec
38	1431	90.9	282	6	ABR74951 Human sec
39	1431	90.9	282	6	ABR94713 Human sec
40	1431	90.9	282	6	ABU13948 Human PRO
41	1431	90.9	282	6	ABU85686 Human PRO
42	1431	90.9	282	6	ABU98846 Novel hum
43	1431	90.9	282	6	ABU98061 Novel hum
44	1431	90.9	282	6	ABU91767 Novel hum
45	1431	90.9	282	6	ABU89460 Human PRO

ALIGNMENTS

RESULT 1
AAH12556
ID AAB12556 standard; protein; 309 AA.

AC AAB12556;

DT 07-NOV-2000 (first entry)

DE Human ovarian carcinoma antigen OBE protein SEQ ID NO:392.

KW Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis; tumour antigen; identification; cytostatic; gene therapy; vaccine.

OS Homo sapiens.

PN WO200036107-A2.

PD 22-JUN-2000.

PE 17-DEC-1999; 99WO-US030270.

PR 17-DEC-1998; 98US-00215681.

PR 17-DEC-1998; 98US-00216003.

PR 23-JUN-1999; 99US-00338933.

PR 24-SEP-1999; 99US-00404879.

PA (CORI-) CORIXA CORP.

PI Mitcham JL, King GE, Algate PA, Frudekis TN;

DR WPI; 2000-431589/37.

PT Immunogenic portion of an ovarian carcinoma protein and the nucleic acid

PT encoding it, useful for the diagnosis, prevention and treatment of

PS cancer, preferably ovarian cancer.

PS Example 2; Page 205-206; 29pp; English.

CC The present invention describes an isolated polypeptide comprising an

CC immunogenic portion of an ovarian carcinoma protein (or its variants).

CC Ovarian carcinoma proteins, and polynucleotides encoding them, have

CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian

CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful

CC for the prevention, diagnosis and treatment of cancer, preferably ovarian

CC cancer. AAH6691 to AAH70077 and AAB12552 to AAB12557 represent human

CC ovarian carcinoma polynucleotides and proteins used in the

CC exemplification of the present invention

XX Example 2; Page 320-321; 408bp; English.
 PS This invention relates to polypeptides comprising an immunogenic portion
 CC of an ovarian carcinoma protein which acts as an immunostimulant and is
 CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations and antigen presenting cells that express
 CC the polypeptides are useful for stimulating an immune response in a
 CC patient and treating ovarian cancer. This sequence represents protein
 CC related to the invention
 XX
 SQ Sequence 309 AA;
 Query Match 100.0%; Score 1574; DB 5; Length 309;
 Best Local Similarity 100.0%; Pred. No. 6.7e-130;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HASAHASGRORLHASASTQIRWEPSPAMASLGQILFWSIIIIIIAGAILIIGFISG 60
 DB 1 HASAHASGRORLHASASTQIRWEPSPAMASLGQILFWSIIIIIIAGAILIIGFISG 60
 QY 61 RHSITVTVASAGNIGEDGILCTFEEDIKLSDIVIQMLEKGYLGIVHEFEKDEISEQ 120
 DB 61 RHSITVTVASAGNIGEDGILCTFEEDIKLSDIVIQMLEKGYLGIVHEFEKDEISEQ 120
 QY 121 DEMFRGRTAVFADQVIVGNASLRKKNVQLTDAGTYKCYIITSKGNANLEYTGAFSMP 180
 DB 121 DEMFRGRTAVFADQVIVGNASLRKKNVQLTDAGTYKCYIITSKGNANLEYTGAFSMP 180
 QY 181 EVNVVDYNASSETLRCEAPRPFQPTVVMASQVDQGANFSEVNTSELSNENTMKNVSV 240
 DB 181 EVNVVDYNASSETLRCEAPRPFQPTVVMASQVDQGANFSEVNTSELSNENTMKNVSV 240
 QY 241 LYNVTINNNTYSCMIENDIAKATGDIKVTSEIKRSHLQILNSKASLCVSSFFAISMALL 300
 DB 241 LYNVTINNNTYSCMIENDIAKATGDIKVTSEIKRSHLQILNSKASLCVSSFFAISMALL 300
 QY 301 PLSPLYMLK 309
 DB 301 PLSPLYMLK 309
 RESULT 4
 ADA08545
 ID ADA08545 standard; protein; 309 AA.
 AC ADA08545;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DB Human ovarian carcinoma polynucleotide O88 protein #1.
 XX
 KM human; gene therapy; ovarian cancer; cancer.
 XX
 OS Homo sapiens.
 XX
 PN US2003091580-A1.
 XX
 PD 15-MAY-2003.
 XX
 PF 17-JUL-2001; 2001US-00907969.
 XX
 FR 18-JUN-2001; 2001US-00884441.
 XX
 PA (MITC/) MITCHAM J L.
 PA (KING/) KING G E.
 PA (ALGA/) ALGATE P A.
 PA (ELIN/) ELING S P.
 PA (REIT/) REITER M W.
 PA (FANG/) FANGER G R.
 PA (REED/) REED S G.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.

PA (HILL/) HILL P.
 PA (ALBO/) ALBONE E.
 XX
 PI Mitcham JL, King GE, Algate PA, Fling SP, Reiter MW, Fanger GR;
 PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
 XX
 DR WPI: 2003-532352/50.
 XX
 PT New isolated 0772p polypeptides and polynucleotides, useful in gene
 PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
 PT cancer.
 XX
 PS Disclosure; SEQ ID NO 392; 371bp; English.
 XX
 CC The invention relates to an isolated 0772p polypeptide, which has the
 CC structure fully defined in the specification. The composition containing
 CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
 CC or antigen presenting cells are useful for stimulating an immune response
 CC and treating ovarian cancer. Detecting the presence of the
 CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
 CC carcinoma cDNAs and protein cDNAs were identified using microarray
 CC technology. The present sequence represents a human ovarian carcinoma
 CC antigen.
 XX
 SQ Sequence 309 AA;
 Query Match 100.0%; Score 1574; DB 7; Length 309;
 Best Local Similarity 100.0%; Pred. No. 6.7e-130;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HASAHASGRORLHASASTQIRWEPSPAMASLGQILFWSIIIIIIAGAILIIGFISG 60
 DB 1 HASAHASGRORLHASASTQIRWEPSPAMASLGQILFWSIIIIIIAGAILIIGFISG 60
 QY 61 RHSITVTVASAGNIGEDGILCTFEEDIKLSDIVIQMLEKGYLGIVHEFEKDEISEQ 120
 DB 61 RHSITVTVASAGNIGEDGILCTFEEDIKLSDIVIQMLEKGYLGIVHEFEKDEISEQ 120
 QY 121 DEMFRGRTAVFADQVIVGNASLRKKNVQLTDAGTYKCYIITSKGNANLEYTGAFSMP 180
 DB 121 DEMFRGRTAVFADQVIVGNASLRKKNVQLTDAGTYKCYIITSKGNANLEYTGAFSMP 180
 QY 181 EVNVVDYNASSETLRCEAPRPFQPTVVMASQVDQGANFSEVNTSELSNENTMKNVSV 240
 DB 181 EVNVVDYNASSETLRCEAPRPFQPTVVMASQVDQGANFSEVNTSELSNENTMKNVSV 240
 QY 241 LYNVTINNNTYSCMIENDIAKATGDIKVTSEIKRSHLQILNSKASLCVSSFFAISMALL 300
 DB 241 LYNVTINNNTYSCMIENDIAKATGDIKVTSEIKRSHLQILNSKASLCVSSFFAISMALL 300
 QY 301 PLSPLYMLK 309
 DB 301 PLSPLYMLK 309
 RESULT 5
 AAY66719
 ID AAY66719 standard; protein; 282 AA.
 AC AAY66719;
 XX
 DT 05-APR-2000 (first entry)
 XX
 DE Membrane-bound protein PRO1291.
 XX
 KM Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
 KM pharmaceutical; receptor immunoadhesin; gene mapping.
 XX
 OS Homo sapiens.
 XX
 PN WO963088-A2.
 XX
 PD 09-DEC-1999.

XX 02-JUN-1999; 99WO-US012252.
PF 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088036P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088730P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088746P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089539P.
PR 17-JUN-1998; 98US-0089592P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090538P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090691P.

PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
PR 01-JUL-1998; 98US-0091360P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096899P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 19-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097611P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-SEP-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.
XX
XX
PA (GEETH) GENENTECH INC.
XX
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
DR WPI, 2000-072883/06.

PS Claim 12; Fig 60; 278bp; English.

XX The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
CC hybridisation probes, and in chromosome and gene mapping

XX Sequence 282 AA;

Query Match 90.9%; Score 1431; DB 4; Length 282;
Best Local Similarity 100.0%; Pred. No. 2.2e-117;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 28 MASIGQLFWSITSIITIIAGALALITGFGISGRHSITVTVASAGNIGEDGILSTCFEP 87
DB 1 MASIGQLFWSITSIITIIAGALALITGFGISGRHSITVTVASAGNIGEDGILSTCFEP 60
QY 88 DIKLSDIVIOMLKEGVGLVHEFEKGEDELSEODEMERGRGTAVFADQVIVGNASLRKNV 147
DB 61 DIKLSDIVIOMLKEGVGLVHEFEKGEDELSEODEMERGRGTAVFADQVIVGNASLRKNV 120
QY 148 QLTDAAGYKCYIITTSKGGKANLEKYGAFSMEPVNDVNASSETLRCEAPRMPPOPTVV 207
DB 121 QLTDAAGYKCYIITTSKGGKANLEKYGAFSMEPVNDVNASSETLRCEAPRMPPOPTVV 180
QY 208 MASQVDOGAFSEVSNTSFEINSENVTKVSVLYNVTINNTYSCMIENDIAKATGDIKV 267
DB 181 MASQVDOGAFSEVSNTSFEINSENVTKVSVLYNVTINNTYSCMIENDIAKATGDIKV 240
QY 268 TESIIRKRSHTQLNSKASLCVSSFPALISWALLPLSPYMLK 309
DB 241 TESIIRKRSHTQLNSKASLCVSSFPALISWALLPLSPYMLK 282

```

RESULT 9

AAB99204 ID AAB99204 standard; protein; 282 AA.

AC AAB99204;

DT 04-SEP-2001 (first entry)

DE Human ovarian tumour-derived antigen O8E #1.

KM Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour;
KM antigen; O8E.

XX Homo sapiens.

PN WO200140269-A2.

PD 07-JUN-2001.

PF 29-NOV-2000; 2000MO-US032520.

PR 30-NOV-1999; 99US-00451651.

PR 22-FEB-2000; 2000US-00510662.

PR 10-MAR-2000; 2000US-00523586.

PR 07-APR-2000; 2000US-00545068.

PR 15-MAY-2000; 2000US-00571025.

PA (CORI-) CORIXA CORP.

PI Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;

DR WPI; 2001-356154/37.

DR N-PSDB; AAH55681.

PT Breast tumor polypeptides and the nucleic acids that encode them, useful

PT for the prevention, diagnosis and treatment of breast cancer.

XX Example 3; Page 190; 221pp; English.

XX The present invention relates to human breast tumour protein coding
CC sequences (see AAH55479-AAH55513, AAH55517-AAH55679 and AAH55682-
CC AAH55762). The breast tumour protein DNA sequences may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the breast tumour protein (e.g. breast cancer.
CC The present sequence is a human ovarian tumour-derived antigen, which was
CC used in an example from the present invention

XX Sequence 282 AA;

Query Match 90.9%; Score 1431; DB 4; Length 282;
Best Local Similarity 100.0%; Pred. No. 2.2e-117;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 28 MASIGQLFWSITSIITIIAGALALITGFGISGRHSITVTVASAGNIGEDGILSTCFEP 87
DB 1 MASIGQLFWSITSIITIIAGALALITGFGISGRHSITVTVASAGNIGEDGILSTCFEP 60
QY 88 DIKLSDIVIOMLKEGVGLVHEFEKGEDELSEODEMERGRGTAVFADQVIVGNASLRKNV 147
DB 61 DIKLSDIVIOMLKEGVGLVHEFEKGEDELSEODEMERGRGTAVFADQVIVGNASLRKNV 120
QY 148 QLTDAAGYKCYIITTSKGGKANLEKYGAFSMEPVNDVNASSETLRCEAPRMPPOPTVV 207
DB 121 QLTDAAGYKCYIITTSKGGKANLEKYGAFSMEPVNDVNASSETLRCEAPRMPPOPTVV 180
QY 208 MASQVDOGAFSEVSNTSFEINSENVTKVSVLYNVTINNTYSCMIENDIAKATGDIKV 267
DB 181 MASQVDOGAFSEVSNTSFEINSENVTKVSVLYNVTINNTYSCMIENDIAKATGDIKV 240
QY 268 TESIIRKRSHTQLNSKASLCVSSFPALISWALLPLSPYMLK 309
DB 241 TESIIRKRSHTQLNSKASLCVSSFPALISWALLPLSPYMLK 282

```

RESULT 10

AAB65242 ID AAB65242 standard; protein; 282 AA.

AC AAB65242;

DT 02-APR-2001 (first entry)

DE Human PRO1291 (UNC659) protein sequence SEQ ID NO:291.

KM Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KM cancer; chromosomal mapping; gene mapping; tissue typing;
KM diagnostic assay.

XX Homo sapiens.

PN WO200073454-A1.

PD 07-DEC-2000.

PF 30-MAR-2000; 2000MO-US008439.

PR 02-JUN-1999; 99MO-US012252.

PR 23-JUN-1999; 99US-0141037P.

PR 07-JUL-1999; 99US-0143048P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 17-AUG-1999; 99US-0146222P.

PR 15-SEP-1999; 99MO-US021090.

PR 08-OCT-1999; 99US-0158663P.

PR 30-NOV-1999; 99MO-US028313.

PR 01-DEC-1999; 99MO-US028301.

CC infections. Sequences of the invention are also used in gene therapy. The
 CC present sequence is human B7-H8 protein. B7-H8 gene is located on
 CC chromosome 1
 XX
 SQ Sequence 282 AA;

Query Match 90.9%; Score 1431; DB 5; Length 282;
 Best Local Similarity 100.0%; Pred. No. 2.2e-117;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLQQLIFWSTIIIIIIIIAGALAIIGFGISGRHSITVTYASAGNIGEDGILICTEP 87
 DB 1 MASLQQLIFWSTIIIIIIIIAGALAIIGFGISGRHSITVTYASAGNIGEDGILICTEP 60
 QY 88 DKLSDIYIOMLKEVGLGVHEFEKGDLSBODEMFGRTVPFDQYVGNASRLKNV 147
 DB 61 DKLSDIYIOMLKEVGLGVHEFEKGDLSBODEMFGRTVPFDQYVGNASRLKNV 120
 QY 148 QLTDAGYKCYIITSKGKNANLEYKTGAFSPMEVNVVDYNASSETLRCEAPRWPQPTVV 207
 DB 121 QLTDAGYKCYIITSKGKNANLEYKTGAFSPMEVNVVDYNASSETLRCEAPRWPQPTVV 180
 QY 208 WASQVDQGANFSEVNTSEFELNSENVTMKVSVLVNVTINNTYSCMIENDIAKATGDIKV 267
 DB 181 WASQVDQGANFSEVNTSEFELNSENVTMKVSVLVNVTINNTYSCMIENDIAKATGDIKV 240
 QY 268 TSEIKRSHLOLNSKASLGVSSFFAISWALLPSPYIMLK 309
 DB 241 TSEIKRSHLOLNSKASLGVSSFFAISWALLPSPYIMLK 282

RESULT 12
 ABG96445
 ID ABG96445 standard; protein; 282 AA.
 XX
 AC ABG96445;

DT 11-DEC-2002 (first entry)
 XX
 DE Human ovarian cancer marker OVB8.
 XX

KM Human; ovarian cancer; marker; cancer; familial history; brain disorder;
 KM central nervous system disorder; bacterial meningitis; vital meningitis;
 KM Alzheimer's disease; Parkinson's disease; cerebral edema; hydrocephalus;
 KM brain herniation; inflammation; encephalitis; testicular disorder;
 KM nonbacterial granulomatous orchitis; connective tissue disorder;
 KM heart disorder; ischemic heart disease; atherosclerosis; neoplasm;
 KM histological type; carcinogenic; ovarian cancer marker.

OS Homo sapiens.
 XX
 PN WO200271928-A2.
 XX

PD 19-SEP-2002.

PF 14-MAR-2002; 2002WO-US007826.

XX
 PR 14-MAR-2001; 2001US-0276025P.
 PR 14-MAR-2001; 2001US-0276026P.
 PR 10-AUG-2001; 2001US-0311732P.
 PR 19-SEP-2001; 2001US-0323580P.
 PR 26-SEP-2001; 2001US-0324967P.
 PR 26-SEP-2001; 2001US-0325102P.
 PR 26-SEP-2001; 2001US-0325149P.

XX
 PA (MILL-) MILLENNIUM PHARM INC.

XX
 PI Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG,
 PI Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vleby PO, Mills GB,
 PI Bast RC, Lu K, Schmandt RE, Zhao X, Glatz K;
 XX
 DR WPI; 2002-723277/78.
 DR N-PSDB; ABS76544.

XX
 PT Assessing whether a patient is afflicted with ovarian cancer, useful in
 PT assessing the stage or progression of the disease, comprises comparing
 PT the expression level of a cancer marker in a sample from a patient and
 PT from a non cancer patient.

PS Disclosure; Page 468-469; 481pp; English.

XX
 CC The present invention relates to a new method for assessing whether a
 CC patient is afflicted with ovarian cancer. The method involves comparing
 CC the expression level of a marker in a patient sample and the normal level
 CC of expression of the marker in a control non-ovarian cancer sample, where
 CC the marker is selected from 363 cancer markers described in the
 CC specification. The method of the invention is useful in diagnosing or
 CC characterizing cancer, in detecting the presence of cancer as early as
 CC possible, and the recurrence of ovarian cancer. The method may also be of
 CC particular use with patients having an enhanced risk of developing
 CC ovarian cancer (e.g. patients having a familial history of ovarian
 CC cancer). The cancer markers may be used in the management and treatment
 CC of e.g. brain and central nervous system disorders (e.g. bacterial and
 CC viral meningitis, Alzheimer's disease or Parkinson's disease), brain
 CC disorders (e.g. cerebral edema, hydrocephalus or brain herniations),
 CC inflammations (e.g. bacterial or viral meningitis or encephalitis),
 CC testicular disorders (e.g. nonbacterial granulomatous orchitis),
 CC connective tissue disorders, or heart disorders (e.g. ischemic heart
 CC disease or atherosclerosis). The compositions and methods may also be
 CC used in assessing the histological type of neoplasm associated with
 CC ovarian cancer, monitoring the progression of ovarian cancer, determining
 CC whether ovarian cancer has metastasized or is likely to metastasize,
 CC selecting a composition for inhibiting ovarian cancer, assessing the
 CC ovarian carcinogenic potential of a compound, or inhibiting ovarian
 CC cancer or at risk of developing ovarian cancer. The present amino acid
 CC sequence represents one of the ovarian cancer markers described in the
 CC invention.

XX
 SQ Sequence 282 AA;

Query Match 90.9%; Score 1431; DB 5; Length 282;
 Best Local Similarity 100.0%; Pred. No. 2.2e-117;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLQQLIFWSTIIIIIIIIAGALAIIGFGISGRHSITVTYASAGNIGEDGILICTEP 87
 DB 1 MASLQQLIFWSTIIIIIIIIAGALAIIGFGISGRHSITVTYASAGNIGEDGILICTEP 60
 QY 88 DKLSDIYIOMLKEVGLGVHEFEKGDLSBODEMFGRTVPFDQYVGNASRLKNV 147
 DB 61 DKLSDIYIOMLKEVGLGVHEFEKGDLSBODEMFGRTVPFDQYVGNASRLKNV 120
 QY 148 QLTDAGYKCYIITSKGKNANLEYKTGAFSPMEVNVVDYNASSETLRCEAPRWPQPTVV 207
 DB 121 QLTDAGYKCYIITSKGKNANLEYKTGAFSPMEVNVVDYNASSETLRCEAPRWPQPTVV 180
 QY 208 WASQVDQGANFSEVNTSEFELNSENVTMKVSVLVNVTINNTYSCMIENDIAKATGDIKV 267
 DB 181 WASQVDQGANFSEVNTSEFELNSENVTMKVSVLVNVTINNTYSCMIENDIAKATGDIKV 240
 QY 268 TSEIKRSHLOLNSKASLGVSSFFAISWALLPSPYIMLK 309
 DB 241 TSEIKRSHLOLNSKASLGVSSFFAISWALLPSPYIMLK 282

RESULT 13
 AAU77766
 ID AAU77766 standard; protein; 282 AA.
 XX
 AC AAU77766;

DT 05-JUN-2002 (first entry)

XX Tumour associated antigenic target polypeptide (TAT) 136.

DE Tumour associated antigenic target polypeptide; TAT; cancer;
 XX

PR 25-JUN-1998; 98US-0090688P.
 PR 25-JUN-1998; 98US-0090689P.
 PR 26-JUN-1998; 98US-0090862P.
 PR 02-JUL-1998; 98US-0091628P.
 PR 10-AUG-1998; 98US-0096012P.
 PR 17-AUG-1998; 98US-0096757P.
 PR 18-AUG-1998; 98US-0096949P.
 PR 18-AUG-1998; 98US-0096959P.
 PR 26-AUG-1998; 98US-0097954P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097979P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 PR 16-SEP-1998; 98US-0100827P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 22-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 08-MAR-1999; 99WO-US010733.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US021252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021194.
 PR 22-DEC-1999; 99WO-US030720.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032378.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX
 XX (GENTECH) GENENTECH INC.
 XX
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX
 XX WPI; 2002-731348/79.
 XX N-PSDB; ABS74407.
 PT New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating sports-related
 PT joint problems, osteoarthritis or rheumatoid arthritis.
 XX
 XX Claim 20; Fig 60; 399pp; English.
 XX
 CC The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing as

CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
 CC extracellular domain of the proteins with their associated signal peptide
 CC or lacking its associated signal peptide. Also included are the nucleic
 CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing an A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
 CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for
 CC identifying agonists or antagonists, for the preparation of a medicament
 CC useful in the treatment of a condition which is responsive to the
 CC proteins, as molecular weight markers for protein electrophoresis
 CC purposes, and as therapeutic agents for treating sports-related joint
 CC problems, nucleic acid defects, osteoarthritis or rheumatoid
 CC arthritis. Nucleic acids encoding the proteins are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to
 CC generate transgenic or knockout animals which are useful in the
 CC development and screening of therapeutic useful reagents, for chromosome
 CC identification, and in gene therapy. The antibody is useful as a
 CC therapeutic agent, in a diagnostic assay and for affinity purification of
 CC the protein from recombinant cell culture natural sources. The present
 CC sequence represents a novel secreted or transmembrane protein of the
 CC invention
 XX
 SQ Sequence 282 AA:
 Query Match 90.9%; Score 1431; DB 5; Length 282;
 Best Local Similarity 100.0%; Pred. No. 2.2e-117;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 28 MASLQQLFWSTISITIIILAGIALITIGFGISGRHSITVTVASAGNIGEDGILSTFEP 87
 DB 1 MASLQQLFWSTISITIIILAGIALITIGFGISGRHSITVTVASAGNIGEDGILSTFEP 60
 QY 88 DIKLSDIVIOMLKEVLAGVHEFKGKDELSEQDMFGRITAVFADQVIVGNASRLKRV 147
 DB 61 DIKLSDIVIOMLKEVLAGVHEFKGKDELSEQDMFGRITAVFADQVIVGNASRLKRV 120
 QY 148 QLTDAQTYKCYITITSGKGNANLEYKGTGAFSPKEVNVVDYNASSETLRCAFPWPQPIYV 207
 DB 121 QLTDAQTYKCYITITSGKGNANLEYKGTGAFSPKEVNVVDYNASSETLRCAFPWPQPIYV 180
 QY 208 WASQVDQGNFSEVNTSEFNLSENVTKVVSVLNVNTINNTNSCMITENDIKAKGDIKV 267
 DB 181 WASQVDQGNFSEVNTSEFNLSENVTKVVSVLNVNTINNTNSCMITENDIKAKGDIKV 240
 QY 268 TSESIKRRSHQLNLSKASLCVSSFPFASWALLPSPYIMLK 309
 DB 241 TSESIKRRSHQLNLSKASLCVSSFPFASWALLPSPYIMLK 282
 RESULT 15
 AAU76536
 ID AAU76536 standard; protein; 282 AA.
 XX
 AC AAU76536;
 XX

Query Match
Best Local Similarity 15.6%; Score 246; DB 4; Length 441;
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

US-09-651-200-4

TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/172909
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/183578
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 4
LENGTH: 441
TYPE: PRT
ORGANISM: Homo sapiens

Query Match
Best Local Similarity 26.2%; Pred. No. 1.2e-16;
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

US-09-651-200-6

TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/172909
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/183578
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 6
LENGTH: 534
TYPE: PRT
ORGANISM: Homo sapiens

Query Match
Best Local Similarity 15.6%; Score 246; DB 4; Length 534;
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

US-09-651-200-6

TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/172909
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/183578
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 6
LENGTH: 534
TYPE: PRT
ORGANISM: Homo sapiens

Query Match
Best Local Similarity 26.2%; Pred. No. 1.6e-16;
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

US-09-651-200-6

TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/172909
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/183578
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 24
LENGTH: 534
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Sequence
US-09-651-200-24

Query Match
Best Local Similarity 15.6%; Score 246; DB 4; Length 534;
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

US-09-651-200-6

TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/172909
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/183578
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 24
LENGTH: 534
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Sequence
US-09-651-200-24

Db 408 VTTS-QMANEGCLFDVHSLRVVLGANGTYSCLVRNPVLQODAHGSVTIT 456

RESULT 8

US-09-651-200-2
 ; Sequence 2, Application US/09651200
 ; Patent No. 6429303
 ; GENERAL INFORMATION:
 ; APPLICANT: Green et al
 ; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
 ; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
 ; FILE REFERENCE: 15966-562 (CUPRA-62)
 ; CURRENT APPLICATION NUMBER: US/09/651,200
 ; PRIOR FILING DATE: 2000-08-30
 ; PRIOR APPLICATION NUMBER: 60/152383
 ; PRIOR FILING DATE: 1999-09-03
 ; PRIOR APPLICATION NUMBER: 60/172909
 ; PRIOR FILING DATE: 1999-12-21
 ; PRIOR APPLICATION NUMBER: 60/183578
 ; PRIOR FILING DATE: 2000-02-18
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: Patent Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 340
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-651-200-2

Query Match 15.6%; Score 245; DB 4; Length 340;
 Best Local Similarity 27.8%; Pred. No. 9.6e-17;
 Matches 72; Conservative 50; Mismatches 101; Indels 36; Gaps 11;

QY 38 SIIISIIILAGALIIIGFGL---SGRHSITVTVA-----AGNIGDGI 80
 Db 12 SILNVLGANGTYSCLVRNPVLQODAHGSVTITPQRPRTGAVEYQVEDPVVALVGTDAT 71
 QY 81 LSCFT--EPULKSDIYIOMLKEGVLGVHEFEKKGKDELSEODEMFRGTAVFADQVTVG 138
 Db 72 LHCSFSPSPGSLQNLINQTLTQKOLVHSTFTEGRD---QSAVANRRTALFPDLAOG 127
 QY 139 NASRLKXVQLTDAGTYKCYITTSKGNANLEYKTA--FSMPENVVDYN---ASSET 192
 Db 128 NASRLKRVRVADGSEFTCF--VSIRDFGSAVSLQVAAPYSKPSMTLEPKKDLRPGDVT 186
 QY 193 LRCEAPRFPQPTVVMASQVDGANSFSEVNTSFEINSEVNTMKVSVLYNVT--INNTYS 251
 Db 187 ITCSYSGYEPAEVFW--QDQGVPLTGNVTT--QMANEGCLFDVHSLRVVLGANGTYS 243
 QY 252 CMENDIAK--ATGDIRVT 268
 Db 244 CLVRNPVLQODAHGSVTIT 262

RESULT 9

US-09-910-174B-28
 ; Sequence 28, Application US/09910174B
 ; Patent No. 6630575
 ; GENERAL INFORMATION:
 ; APPLICANT: Coyle, Anthony J.
 ; APPLICANT: Fraser, Christopher C.
 ; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
 ; TITLE OF INVENTION: Family and Uses Thereof
 ; FILE REFERENCE: 35800/236924
 ; CURRENT APPLICATION NUMBER: US/09/910,174B
 ; PRIOR FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: US 09/620,461
 ; PRIOR FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 28

; LENGTH: 315
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-910-174B-28

Query Match 15.2%; Score 238.5; DB 4; Length 315;
 Best Local Similarity 26.9%; Pred. No. 4e-16;
 Matches 65; Conservative 46; Mismatches 112; Indels 19; Gaps 7;

QY 37 WSIIISIIILAGALIIIGFGLSGRHSITVTVAAGNIGEDGILCTF--EPDIKLSDI 94
 Db 5 WGGSPSVGCVRRLAG-VLCICLTGAVEYQVEDPVVALVDTATLRCSFSPGSLAQL 63
 QY 95 VIOMLKEGVLGVHEFEKKGKDELSEODEMFRGTAVFADQVTVGNASRLKXVQLTDAGT 134
 Db 64 NLTMQLTDKQLVHSTFTEGRD---QSAVANRRTALFPDLVQGNASRLKRVRVYDEGS 119
 QY 155 YKCYITTSKGNANLEYKTAFSMPENVVDYN---ASSETLRCEAPRFPQPTVVA 209
 Db 120 YTCFVSIQDPDSAAVSLQVAAPYSKPSMTLEPKKDLRPGNMVITTCSSYGYEAEVFW- 178
 QY 210 SQVDGANSFSEVNTSFEINSEVNTMKVSVLYNVT--INNTYS CMENDIAK--ATGDIR 266
 Db 179 ---KDGQGVPLTGNVTSQMANERGLFDVHSLRVVLGANGTYSCLVRNPVLQODAHGSVT 235
 QY 267 VT 268
 Db 236 IT 237

RESULT 10

US-09-620-461-28
 ; Sequence 28, Application US/09620461
 ; Patent No. 6635750
 ; GENERAL INFORMATION:
 ; APPLICANT: Coyle, Anthony J.
 ; APPLICANT: Fraser, Christopher C.
 ; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
 ; TITLE OF INVENTION: Family and Uses Thereof
 ; FILE REFERENCE: 5800-149
 ; CURRENT APPLICATION NUMBER: US/09/620,461
 ; CURRENT FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 28
 ; LENGTH: 315
 ; TYPE: PRT
 ; ORGANISM: Mus
 US-09-620-461-28

Query Match 15.2%; Score 238.5; DB 4; Length 315;
 Best Local Similarity 26.9%; Pred. No. 4e-16;
 Matches 65; Conservative 46; Mismatches 112; Indels 19; Gaps 7;

QY 37 WSIIISIIILAGALIIIGFGLSGRHSITVTVAAGNIGEDGILCTF--EPDIKLSDI 94
 Db 5 WGGSPSVGCVRRLAG-VLCICLTGAVEYQVEDPVVALVDTATLRCSFSPGSLAQL 63
 QY 95 VIOMLKEGVLGVHEFEKKGKDELSEODEMFRGTAVFADQVTVGNASRLKXVQLTDAGT 154
 Db 64 NLTMQLTDKQLVHSTFTEGRD---QSAVANRRTALFPDLVQGNASRLKRVRVYDEGS 119
 QY 155 YKCYITTSKGNANLEYKTAFSMPENVVDYN---ASSETLRCEAPRFPQPTVVA 209
 Db 120 YTCFVSIQDPDSAAVSLQVAAPYSKPSMTLEPKKDLRPGNMVITTCSSYGYEAEVFW- 178
 QY 210 SQVDGANSFSEVNTSFEINSEVNTMKVSVLYNVT--INNTYS CMENDIAK--ATGDIR 266
 Db 179 ---KDGQGVPLTGNVTSQMANERGLFDVHSLRVVLGANGTYSCLVRNPVLQODAHGSVT 235
 QY 267 VT 268

Db 236 IT 237

RESULT 11

US-09-910-174B-18

; Sequence 18, Application US/09910174B
; Patent No. 6630575

; GENERAL INFORMATION:

; APPLICANT: Coyle, Anthony J.

; APPLICANT: Frazer, Christopher C.

; APPLICANT: Manning, Stephen

; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7

; FILE REFERENCE: 35800/236924

; CURRENT APPLICATION NUMBER: US/09/910,174B

; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 09/620,461

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 18

; LENGTH: 513

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-910-174B-18

Query Match

14.2%; Score 223; DB 4; Length 513;

Best Local Similarity 26.4%; Pred. No. 3.4e-14;
Matches 69; Conservative 44; Mismatches 108; Indels 40; Gaps 10;

```
QY 62 HSITVTYVASAGNI---GEGDILSCTPEPDIKLSDIVIQWKEGVGLVHEFEKQDEL 117
DB 27 HSAQSVLGPSPILAMWGEDADLPCHLFPMTSAETMELKXWSSSLRQVNVYADGKEVE 86
QY 118 SEQDEMERKRTAVFADQIVGNASLRKXVQLTDAGTYCYIITSKGNANLEXYTGAF 177
DB 87 DRQSAFYRGRTSLIRDGITAGCAALRHNVTASDSGKLYCYFQDGFYEKALVELKVAL 146
QY 178 SMPEVNVV---YNASSETLRCEAPRPFPQPTVWNASQVQGANFSEVNTSELSSENT 234
DB 147 G-SDLAHVYKYGKDGSIHECRSTGWYPOQIOWSN--NKGNN---IPVEAPVYADGVG 200
QY 235 MKVY--SVLYNVTINNYSQMIENDIAKATGDIKVTSEIKRSHQLINASKASLCVSS- 291
DB 201 LYAVASVYMRGSSGEGVSGCTI-----RSSILGLEKTAISISIADP 240
QY 292 FF--AISW--ALLPSPYIML 308
DB 241 FFRSAQRWIALARTLPVILL 261
```

RESULT 12

US-09-620-461-18

; Sequence 18, Application US/09620461

; Patent No. 6635750

; GENERAL INFORMATION:

; APPLICANT: Coyle, Anthony J.

; APPLICANT: Frazer, Christopher C.

; APPLICANT: Manning, Stephen

; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7

; FILE REFERENCE: 5800-149

; CURRENT APPLICATION NUMBER: US/09/620,461

; CURRENT FILING DATE: 2000-07-20

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 18

; LENGTH: 513

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-620-461-18

Query Match

14.2%; Score 223; DB 4; Length 513;

Best Local Similarity 26.4%; Pred. No. 3.4e-14;
Matches 69; Conservative 44; Mismatches 108; Indels 40; Gaps 10;

```
QY 62 HSITVTYVASAGNI---GEGDILSCTPEPDIKLSDIVIQWKEGVGLVHEFEKQDEL 117
DB 27 HSAQSVLGPSPILAMWGEDADLPCHLFPMTSAETMELKXWSSSLRQVNVYADGKEVE 86
QY 118 SEQDEMERKRTAVFADQIVGNASLRKXVQLTDAGTYCYIITSKGNANLEXYTGAF 177
DB 87 DRQSAFYRGRTSLIRDGITAGCAALRHNVTASDSGKLYCYFQDGFYEKALVELKVAL 146
QY 178 SMPEVNVV---YNASSETLRCEAPRPFPQPTVWNASQVQGANFSEVNTSELSSENT 234
DB 147 G-SDLAHVYKYGKDGSIHECRSTGWYPOQIOWSN--NKGNN---IPVEAPVYADGVG 200
QY 235 MKVY--SVLYNVTINNYSQMIENDIAKATGDIKVTSEIKRSHQLINASKASLCVSS- 291
DB 201 LYAVASVYMRGSSGEGVSGCTI-----RSSILGLEKTAISISIADP 240
QY 292 FF--AISW--ALLPSPYIML 308
DB 241 FFRSAQRWIALARTLPVILL 261
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RESULT 13

US-08-724-394A-4

; Sequence 4, Application US/08724394A

; Patent No. 5872237

; GENERAL INFORMATION:

; APPLICANT: Feder, John N.

; APPLICANT: Krommal, Gregory S.

; APPLICANT: Lauery, Peter M.

; APPLICANT: Ruddy, David A.

; APPLICANT: Thomas, Winston

; APPLICANT: Tsuchihashi, Zenta

; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESS: TOWNSEND and TOWNSEND and CREW LLP

; STREET: Two Embarcadero Center, 8th floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/724,394A

; FILING DATE: 01-OCT-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitts, Renee A.

; REGISTRATION NUMBER: 35,136

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-576-0200

; TELEFAX: 415-576-0300

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 540 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Region

; LOCATION: 1..540

; OTHER INFORMATION: /note= "BTFS"

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 16:17:11 ; Search time 21 Seconds
(without alignments)
1415.390 Million cell updates/sec

Title: US-09-827-271-392

Perfect score: 1574

Sequence: 1 HASAHASGRORQHASTQI.....SSFFAISMLPLSPYIMLK 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	219.5	13.9	526	2 A37821	butyrophillin - bov
2	211.5	13.4	526	2 S70587	butyrophillin precu
3	171.5	10.9	487	2 S65133	butyrophillin - mou
4	168.5	10.7	391	2 T09058	butyrophillin homol
5	163.5	10.4	299	2 I46680	CD86 precursor - t
6	153	9.7	275	2 UC7604	CD86 spliced varia
7	151	9.6	339	2 T28138	Ig V-region-like B
8	150.5	9.6	340	2 T28137	Ig V-region-like B
9	150	9.5	247	2 A55717	myelin/oligodendro
10	147.5	9.4	339	1 A48754	B7-2 antigen - hum
11	147.5	9.4	330	2 I46691	CD86 precursor - t
12	147.5	9.3	218	2 B47712	myelin/oligodendro
13	146.5	9.3	372	2 C39371	Ig V-region-like B
14	146	9.3	398	2 A39371	Ig V-region-like B
15	144	9.1	247	2 S58394	myelin/oligodendro
16	143.5	9.1	309	2 I49522	Gene B7-2 protein
17	140.5	8.9	246	2 A47712	myelin/oligodendro
18	135	8.6	761	1 UCHONG	neural cell adhesi
19	134.5	8.5	503	1 UC5287	SHP substrate-1 pr
20	133	8.4	1091	1 IJCHNL	neural cell adhesi
21	132.5	8.4	853	1 IJBNOC	neural cell adhesi
22	130.5	8.3	725	1 SI9247	neural cell adhesi
23	130.5	8.3	1033	2 SI9247	cell adhesion prot
24	130.5	8.3	1115	1 IUMSNL	neural cell adhesi
25	128.5	8.2	858	1 IJRNKC	neural cell adhesi
26	127	8.1	946	1 A47299	ror-related recept
27	126.5	8.0	765	2 C42632	cell adhesion mole
28	126.5	8.0	812	2 B42632	cell adhesion mole
29	126.5	8.0	932	2 A42632	cell adhesion mole

30	126.5	8.0	1088	1 IJXNLT	neural cell adhesi
31	125.5	8.0	1018	2 UC4211	neural adhesion pr
32	124	7.9	309	2 I49503	B-lymphocyte activ
33	123.5	7.8	725	2 JE0099	neural cell adhesi
34	123.5	7.8	5175	2 T20992	hypothetical prote
35	123.5	7.8	5198	2 T43290	hemiscentin precu
36	122.5	7.8	871	1 I46696	protein-tyrosine k
37	122.5	7.8	881	1 I46697	protein-tyrosine k
38	121.5	7.7	1612	2 T30805	protein-tyrosine k
39	121	7.7	321	2 I54766	ducal protein - mo
40	121	7.7	365	2 UC7780	B-lymphocyte activ
41	121	7.7	1091	2 S01998	coxsackie- and ade
42	120	7.6	215	2 A57843	contactin precurs
43	120	7.6	388	2 A45803	sodium channel bet
44	120	7.6	333	2 A31923	B-cell-restricted
45	118	7.5	321	2 D39371	amalgam protein pr
					Ig V-region-like B

ALIGNMENTS

RESULT 1

A37821

butyrophillin - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 05-Nov-1999

C:Accession: A37821

R:Jack, L.J.W.; Mather, I.H.

J. Biol. Chem. 265, 14481-14486, 1990

A:Title: Cloning and analysis of cDNA encoding bovine butyrophillin, an apical glycoprotein

A:Reference number: A37821; MUID:90354441; PMID:2387867

A:Accession: A37821

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-526 <OAC>

A:Cross-references: GB:M3551; NID:91763685; PIDN:AAB39766.1; PID:9162773

C:Keywords: transmembrane protein

Query Match 13.9%; Score 219.5; DB 2; Length 526;

Best Local Similarity 25.0%; Pred. No. 4.5e-09;

Matches 49; Conservative 48; Mismatches 94; Indels 5; Gaps 4;

QY 75 IGEDELISCTFEEDIKLSDIVQLKEGVGLVHEFEKSKDELSEDEMERGRFAVADQ 134

Db 42 VGEDELIPCLSPNVSAGKGMELRMFEKXSPAVFVSREGQEGEMAEYRGRVSLVEDH 101

QY 135 VIVGNASLRLKXVQLTDACTYKCYITTSKGGKGNALPYTGAF-SMPEVNVVDYNASSE-T 192

Db 102 IIEGSAVARIOEVKASDDGEYRCFPRQDYEAEIVHLKVAALGSDPHISMKVQESGEIQ 161

QY 193 LRCEAPRPFQPTVWASOVDOGANFSEVSNFSFELNSENVMKVVSIVYNTVNTYSG 252

Db 162 LECTSVGWTFPEQVQW-RTHRGEFPSPMSSEKNDPEBGLFTVRASVITTRDSMKV-SC 218

QY 253 MIENDIAKATGDIKVT 268

Db 219 CIRNILLQGEKDEVEVS 234

RESULT 2

S70587

butyrophillin precursor - human

C:Species: Homo sapiens (man)

C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000

C:Accession: S70587

R:Taylor, M.R.; Peterson, J.A.; Ceriani, R.L.; Couto, J.R.

Biochim. Biophys. Acta 1306, 1-4, 1996

A:Title: Cloning and sequence analysis of human butyrophillin reveals a potential recep

A:Reference number: S70587; MUID:96201696; PMID:8611614

A:Accession: S70587

A>Status: preliminary

A:Molecule type: mRNA

	Query Match	9.6%	Score 151;	DB 2;	Length 339;
	Best Local Similarity	21.7%	Pred. No. 0.00044;		
	Matches	56;	Conservative 46;	Mismatches 99;	Indels 66; Gaps 10;
QY	63	SITTTTAAAGNIGEDDILCTFEP--DIKSIDIVIQWLKCGVLGTHAEFKEGKDELSEQ	120		
		:::::			
Db	42	SLRTAL----VQDVLRQLCLPCKAWSSD--IRNIQRTSGVFHYHONGED--LEQ	92		

RESULT 9
A55717
Myelin/oligodendrocyte glycoprotein precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 08-Oct-1999
C/Accession: A55717; C47712
R/Daubas, P.; Phan-Dinh, D.; Dautigny, A.
Genomics 23, 36-41, 1994
A/Title: Structure and polymorphism of the mouse myelin/oligodendrocyte glycoprotein gene
A/Reference number: A55717; MUID:95130110; PMID:7829100
A/Accession: A55717
A/Molecule type: DNA
A/Residues: 1-247 <DAU>
A/Cross-references: GB:L29498
R/Pham-Dinh, D.; Matreel, M.G.; Nussbaum, J.L.; Rousset, G.; Pontarotti, P.; Roedel, N.
Proc. Natl. Acad. Sci. U.S.A. 90, 7999-7994, 1993
A/Title: Myelin/Oligodendrocyte glycoprotein is a member of a subset of the immunoglobulin
A/Reference number: A47712; MUID:93376728; PMID:8367453
A/Accession: C47712
A/Molecule type: mRNA
A/Residues: 30-95/'E',97-247 <PHA>
A/Cross-references: GB:L20942; NID:G339588; PIDD:AAA03180.1; PID:G339589

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Db      66 NEVYLGEKEDSVHASKYMGRTSFSD-----SWTLRLAHNIQIDKGLYQCIIHHKRPYGM 120
Qy      167 ----NANLEKTKGA-FSMPEV-----NVDYASSETLACEAPRMFPQPTVYVWASQVDOGAN 217
Db      121 IRHQNNSSELSVLANSFQPEIVPISNITENVYI-NLTCCSIHGYPEP-----166
Qy      218 FSEVSNTPSELSSENVTKV-----VSVLVNTI-----NNTYSCMIEN 256
Db      167 ----KKMSVLLRFTKNSITLKDGIQMSQDNVTELHYDSISLSVSPDVTSNMTIFCLLET 222
Qy      257 DIKATGDIVNTSEIR--RSHQLINS--KASLCVSSFFPAISW 297
Db      223 DKRLTSSPFSIEHEDQPEPDHPIWITAVLPTVLCVMFCILW 268

RESULT 11
I46691
C/D86 precursor - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 23-Jul-1999
C/Accession: I46691
R/Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A/Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule
A/Reference number: I46689; MUID:95369849; PMID:7642234
A/Accession: I46691
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-330 <ISO>
A/Cross-references: GB:D49842; NID:g755098; PIND:BA08642.1; PID:g755099
C/Superfamily: B7-2 antigen

Query Match      9.4%; Score 147.5; DB 2; Length 330;
Best Local Similarity 24.0%; Pred. No. 0.00078;
Matches 59; Conservative 44; Mismatches 80; Indels 63; Gaps 11;

Qy      38 SIISIIITLGAIALIIIGFISGRHSITVTVASAGTIGDGLISCTF--EPDIKLSIV 95
Db      12 TVPMALLISGAASLIR-----QAVFNKTADLPCCPTNSQGRSISELV 54
Qy      96 IOWLKEGVGLVHAFPEKGEDELSEODEMFGRATVAFADQIVGNASRLRNVOITDAGTY 155
Db      55 VFMQDQERL-VLYELFLGREKPDNVDPKYGRTSF--DQ---ESWNIQLHNVQIKKGVY 109
Qy      156 KCVIITSKGG-----NANLEKTKGA-FSMPEVNVQYNA--SSETLRCEAPRMFPQPTV 206
Db      109 QCEVHHRGAAGLPIVYQNNSELSVLNFTQPEITLISNITRNAAINLTCCSVQGYEPK 168
Qy      207 VMSQVDQGANFSEVSNTPSELSSENVTKV-----VSVLVNTINNTYSCMIEN 256
Db      169 MF-----FVLKTEHATTEYDGVTEKSDQNVIGLNIISIG--STFFSD 209

Qy      257 DIKAT 262
Db      210 DIRMAT 215

RESULT 12
B47712
C/myelin/Oligodendrocyte glycoprotein - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 21-Jan-1994 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C/Accession: B47712
R/R/Pham-Dinh, D.; Mattei, M.G.; Nussbaum, J.L.; Roussel, G.; Pontarotti, P.; Roeckel, N.;
Proc. Natl. Acad. Sci. U.S.A. 90, 7990-7994, 1993
A/Title: Myelin/Oligodendrocyte glycoprotein is a member of a subset of the immunoglobulin
A/Reference number: A47712; MUID:93376728; PMID:8367453
A/Accession: B47712
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-218 <PNA>
A/Experimental source: brain
A/Note: Sequence extracted from NCBI backbone (NCBIP.137804)

```

C:Genetics: A:Gene: MOG
C:Function: A:Description: may be involved in lipid interaction; may be involved in cell-cell commu
C:Keywords: glycoprotein; myelin; transmembrane protein
F:1-118/Product: myelin/oligodendrocyte glycoprotein #status predicted <MNT>
F:122-150/Domain: transmembrane #status predicted <TM1>
F:175-200/Domain: transmembrane #status predicted <TM2>
F:331/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 9.3%; Score 147; DB 2; Length 218;
Best Local Similarity 28.3%; Pred. No. 0.0005;
Matches 28; Conservative 24; Mismatches 47; Indels 0; Gaps 0;

QY 75 IGEEDIIISTEPEDIKSDIYIOWLKEGVLGVHFEKGEDELSEGEEMRGRRAVADQ 134
Db 16 VGDEELPECRISPCKNKAAGMEVGRSPFSRVHLHYNRKQDAEAPERYKTELLKES 75
QY 135 VIVGNASLRKNNVQITDAGTYKCYIITSKGNANLEYK 173
Db 76 IGEKVVALRIQNVAFSPDEGYTCFFRHSYGEEAAVELK 114

RESULT 13
C39371
Ig V-region-like B-G antigen 11/4 precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 23-Mar-1993
C:Accession: C39371
R:Miller, M.M.; Goto, R.; Young, S.; Chirivella, J.; Hawke, D.; Miyada, C.G.
Proc. Natl. Acad. Sci. U.S.A. 88, 4377-4381, 1991
A:Title: Immunoglobulin variable-region-like domains of diverse sequence within the majd
A:Reference number: A39371; MUID:91239571; PMID:1903541
A:Accession: C39371
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-372 <MID>
A:Cross-references: GB:M61861

Query Match 9.3%; Score 146.5; DB 2; Length 372;
Best Local Similarity 20.7%; Pred. No. 0.0011;
Matches 59; Conservative 51; Mismatches 88; Indels 87; Gaps 9;

QY 63 SITTTVASAGNIGEDGILSTCFEPDIKLSDIYIOWLKEGYLVHFEKGEKDELSODE 122
Db 42 SLRYVAL-----VQGDVVLRLCHLCPCKDAMFLDIRMILORSSGFVHHYQNGVD-LGQMER 95
QY 123 MFRGTAFAFDQVIVGNASLRKNNVQITDAGTYKCYIITSKGNANLEYK----- 173
Db 96 YKGRTELLRGLVDGNIDLKITAVSTSDSSYGCAVQDGDGYADAVVDLEVPSPQIV 154
QY 174 -----TGAF-----SMPEVNVYNASSETLRCEA 197
Db 155 HPWKVALAVVTIIVGSEVINVFLCRKKAQSRRLKRDALAEIDELISALNLR----- 211
QY 198 PRWPPQPRVWASQVDDQANSEVSNTSFEIENSVYMKV-----VGVLY 242
Db 212 -----QLASKKNENADEVEDNSLKKDCBEMSGVADIKELAAKLEEYIAVNR 262
QY 243 NVITNNYSCMIENDIAKATGDIKYTESEIR-----RSHLQLLNK 284
Db 263 NVKLN-----IAAKLAQOTKELEKQHSQFRRHQRMDLSAVNQK 302

RESULT 14
A39371
Ig V-region-like B-G antigen 14/8 precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 01-Dec-2000
C:Accession: A39371; B39371
R:Miller, M.M.; Goto, R.; Young, S.; Chirivella, J.; Hawke, D.; Miyada, C.G.
Proc. Natl. Acad. Sci. U.S.A. 88, 4377-4381, 1991
A:Title: Immunoglobulin variable-region-like domains of diverse sequence within the majd

```
A;Reference number: A39371; MUID:91239571; PMID:1903541  
A;Accession: A39371  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-398 <MIT>  
A;Cross-references: GB:M61860; NID:g211241; PIDN:AAA48619.1; PTD:g211243  
A;Accession: B39371  
A>Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-385,387-398 <MI2>  
A;Cross-references: GB:M61864; NID:g211264; PIDN:AAA48630.1; PTD:g211266
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Query Match 9.3%; Score 146; DB 2; Length 398;

Best Local Similarity 33.1%; Pred.No.0.0013;

Matches 40; Conservative 25; Mismatches 42; Indels 14; Gaps 7;

```
Cy            63 SIIVTVVASANIGEDGILCTFEP--DIKSDIYQWLKEGVLGIVEHFKRGKDLSIQ 120  
             ||:||::||:|::||:||||::|||::|||::|||::|||:  
Db            42 SLRITAI-----VGQDVVLRCHSLPCKDVRND--IRMTQQSSRLVHYHRNGVD-LGGM 93  
  
Cy            121 DEMFRGTAVADQVIWNASLRLKNVOLTPAGTYKYIIITSKGKNA--NLTEYKTAFS 178  
             ||::||::|||::|||::|||::|||::|||::|||::|||:  
Db            94 EE-YKGRTELRLDGSLDNLDLRITAAYTSSSGSYSCAWQDDAAVAEAVVNLE-V-SDPES 151  
  
Cy            179 M 179  
Db            152 M 152
```

Query Match 9.1%; Score 144; DB 2; Length 247;

RESULT 15

558394

myelin/oligodendrocyte glycoprotein precursor - human

C:Species: Homo sapiens (man)

C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999

A:Accession: S58394; S78430; S78431; S56513

R:Hilton, A.A.; Slavin, A.U.; Hilton, D.T.; Bernard, C.C.A.

J:Neurochem. 65, 309-318, 1995

A:Title: Characterization of cDNA and genomic clones encoding human myelin oligodendrocyte glycoprotein

A:Reference number: S58394; MUID:95310543; PMID:7790876

A:Accession: S58394

A:Molecule type: mRNA

A:Residues: 1-247 <H1>

A:Cross-references: EMBL:X74511; NID:G984146; PIDN:CAAS2617.1; PID:G984147

A:Experimental source: adult medulla

A:Accession: S78430

A:Molecule type: mRNA

A:Residues: 1-197, 'GKRRHV' <H1>

A>Note: truncated protein is probably not functionally active

A:Accession: S78431

A:Molecule type: DNA

A:Residues: 1-247 <H1>

A:Cross-references: GB:X74511; NID:G984146; PIDN:CAAS2617.1; PID:G984147

J:Pham-Dinh, D.; Alliquant, B.; Ruberg, M.; Della Gaspera, B.; Nussbaum, J.L.; Davignon, J. Neurochem. 63, 2355-2356, 1994

A:Title: Characterization and expression of the cDNA coding for the human myelin/oligodendrocyte glycoprotein

A:Reference number: S56513; MUID:95054056; PMID:7964757

A:Accession: S56513

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-247 <RS>

A:Cross-references: GB:S73472; NID:G688175; PID:G688176

C:Genetics:

A:Gene: MOG

A:Function:

A:Description: may be involved in lipid interaction; may be involved in cell-cell communication

C:Keywords: alternative splicing; glycoprotein; myelin; transmembrane protein

F:1-39/Domain: signal sequence #status predicted <SIG>

F:30-247/Product: myelin/oligodendrocyte glycoprotein #status predicted <WAT>

F:151-179/Domain: transmembrane #status predicted <TM1>

F:204-229/Domain: transmembrane #status predicted <TM2>

F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Best Local Similarity 20.8%; Pred. No. 0.001;
Matches 49; Conservative 39; Mismatches 80; Indels 68; Gaps 6;
QY 28 MASLGQILFMSIISIITILL-----AGAILIIGFGISGRHSITVTVASAGNIGED 78
Db 1 MASLSRPSLPSCLSFILLLLQVSSSVAGQFRV-----ICPRHPIRAL-----VGDE 48
QY 79 GILSTFEPDIXSDIYIOWIKBGVLGLVHEFKKQDELSEODEMFRGRTAVPADQYIVG 138
Db 49 VELPCRIISPGKNATGMEGVMTIRPPFSRVVHLVNRNGKDDGDQDAPEYRGRTELLKDAIGEG 108
QY 139 NASLRKNNVQITDAGTYKCYIITSKGNANLEYKTGAFSPMEYVNVYNNASSETLRCEAP 138
Db 109 KVTLRIRNVRFSDSGFTCFPRDHSYQBEAAME-----LKVEDP 147
QY 199 RWPPOPTVWVASQVDQANFSEVSNTSFEIENSEVTMKVVSV-LYNYTINNNTYSCM 253
Db 148 FYWVSPGVL-----VLLAVLPVLLIQITVGIVFCL 178

Search completed: May 11, 2004, 16:23:29
Job time : 21 secs

Db 181 WASQVDOGANFSEVSNFSFELNSENVTMKVSVLYNTVNTNNTYSCMIENDIAKATGDIKV 240
 QY 268 TSEIKRRSHIQLNRSKSLCVSSFFAISWALLPLSPYLMK 309
 Db 241 TSEIKRRSHIQLNRSKSLCVSSFFAISWALLPLSPYLMK 282

RESULT 2

Q9H6B2 PRELIMINARY; PRT; 282 AA.
 AC Q9H6B2
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein FLJ22418.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]

RE SEQUENCE FROM N.A.
 RA Kwabata A., Hiki T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Ota T., Suzuki Y., Oiyasahi M., Nishi T., Shibahara T.,
 RA Tanaka T., Nakamura Y., Isega T., Sugano S.;
 RT "NDO human cDNA sequencing project."
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK026071; BAB15349.1; -
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR SMART; SM00409; IG, 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 282 AA; 30893 MW; 6F9066999A1E9DB4 CRC64;

Query Match 90.5%; Score 1425; DB 4; Length 282;
 Best Local Similarity 99.6%; Pred. No. 3.1e-108;
 Matches 281; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 MASLGQILFWSIIIIIIIIAGATALLIFGIGSGRHSITVTVASAGNIGEDGILSCFEP 87
 Db 1 MASLGQILFWSIIIIIIIIAGATALLIFGIGSGRHSITVTVASAGNIGEDGILSCFEP 60
 QY 88 DIKLSDIVIOWLKEGVGLVHEFEKDELSQDEMERGRATVADQVYGNASLRKNV 147
 Db 61 DIKLSDIVIOWLKEGVGLVHEFEKDELSQDEMERGRATVADQVYGNASLRKNV 120
 QY 148 QLTDAAGTYKCYIITSGKGNANLEYKTGAFSPMEVNDVNASSETLRCEAPRMPPTTV 207
 Db 121 QLTDAAGTYKCYIITSGKGNANLEYKTGAFSPMEVNDVNASSETLRCEAPRMPPTTV 180
 QY 208 WASQVDOGANFSEVSNFSFELNSENVTMKVSVLYNTVNTNNTYSCMIENDIAKATGDIKV 267
 Db 181 WASQVDOGANFSEVSNFSFELNSENVTMKVSVLYNTVNTNNTYSCMIENDIAKATGDIKV 240
 QY 268 TSEIKRRSHIQLNRSKSLCVSSFFAISWALLPLSPYLMK 309
 Db 241 TSEIKRRSHIQLNRSKSLCVSSFFAISWALLPLSPYLMK 282

RESULT 3

Q7TPH5 PRELIMINARY; PRT; 283 AA.
 AC Q7TPH5
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE B7S1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]

RE SEQUENCE FROM N.A.

FX MEDLINE=22703430; PubMed=12618166;
 RA Prasad D.V., Richards S., Mai X.W., Dong C.;
 RT "B7S1, a novel B7 family member that negatively regulates T cell
 RT activation."
 RL Immunity 18:863-873 (2003).
 DR EMBL; AY322147; AAP8965.1; -
 SQ SEQUENCE 283 AA; 30847 MW; A97F17461857850B CRC64;

Query Match 80.1%; Score 1261.5; DB 11; Length 283;
 Best Local Similarity 88.0%; Pred. No. 6.9e-95;
 Matches 249; Conservative 13; Mismatches 20; Indels 1; Gaps 1;

QY 28 MASLGQILFWSIIIIIIIIAGATALLIFGIGSGRHSITVTVASAGNIGEDGILSCFEP 87
 Db 1 MASLGQILFWSIIIIIIIIAGATALLIFGIGSGRHSITVTVASAGNIGEDGILSCFEP 60
 QY 88 DIKLSDIVIOWLKEGVGLVHEFEKDELSQDEMERGRATVADQVYGNASLRKNV 147
 Db 61 DIKLSDIVIOWLKEGVGLVHEFEKDELSQDEMERGRATVADQVYGNASLRKNV 120
 QY 148 QLTDAAGTYKCYIITSGKGNANLEYKTGAFSPMEVNDVNASSETLRCEAPRMPPTTV 207
 Db 121 QLTDAAGTYKCYIITSGKGNANLEYKTGAFSPMEVNDVNASSETLRCEAPRMPPTTV 180
 QY 208 WASQVDOGANFSEVSNFSFELNSENVTMKVSVLYNTVNTNNTYSCMIENDIAKATGDIKV 267
 Db 181 WASQVDOGANFSEVSNFSFELNSENVTMKVSVLYNTVNTNNTYSCMIENDIAKATGDIKV 240
 QY 268 TSEIKRRSHIQLNRSKSLCVSSFFAISWALLPLSPYLMK 309
 Db 241 TSEIKRRSHIQLNRSKSLCVSSFFAISWALLPLSPYLMK 283

RESULT 4

Q7TPS5 PRELIMINARY; PRT; 283 AA.
 AC Q7TPS5
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Immune costimulatory protein B7-H4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]

RE SEQUENCE FROM N.A.
 RA STRAIN=BALB/c;
 RA Sica G.L., Choi I.-H., Zhu G., Tamada K., Wang S.-D., Tamura H.,
 RA Chapoval A.I., Flies D.B., Bajorath J., Chen L.;
 RT "Immune inhibition by mouse B7-H4."
 RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY280973; AAP37284.1; -
 SQ SEQUENCE 283 AA; 30875 MW; 7E2F174618578519 CRC64;

Query Match 79.9%; Score 1257.5; DB 11; Length 283;
 Best Local Similarity 87.6%; Pred. No. 1.5e-94;
 Matches 246; Conservative 13; Mismatches 21; Indels 1; Gaps 1;

QY 28 MASLGQILFWSIIIIIIIIAGATALLIFGIGSGRHSITVTVASAGNIGEDGILSCFEP 87
 Db 1 MASLGQILFWSIIIIIIIIAGATALLIFGIGSGRHSITVTVASAGNIGEDGILSCFEP 60
 QY 88 DIKLSDIVIOWLKEGVGLVHEFEKDELSQDEMERGRATVADQVYGNASLRKNV 147
 Db 61 DIKLSDIVIOWLKEGVGLVHEFEKDELSQDEMERGRATVADQVYGNASLRKNV 120
 QY 148 QLTDAAGTYKCYIITSGKGNANLEYKTGAFSPMEVNDVNASSETLRCEAPRMPPTTV 207
 Db 121 QLTDAAGTYKCYIITSGKGNANLEYKTGAFSPMEVNDVNASSETLRCEAPRMPPTTV 180
 QY 208 WASQVDOGANFSEVSNFSFELNSENVTMKVSVLYNTVNTNNTYSCMIENDIAKATGDIKV 267

ID	Q8K091	PRELIMINARY	PRT	283 AA
AC	Q8K091			
DT	01-OCT-2002	(TREMBLrel. 22, Created)		
DT	01-OCT-2002	(TREMBLrel. 22, last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25, last annotation update)		
DE	Similar to hypothetical protein FLJ22418.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	Tissue=Uterus;			
RA	Strausberg R.			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC032925; AAH32925.1; ..			
DR	InterPro; IPR003599; IG_			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003598; IG_c2.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00409; Ig_1.			
DR	SMART; SM00408; IGc2.1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
KW	Hypothetical protein; Immunoglobulin domain.			
SQ	SEQUENCE 283 AA; 30801 MW; 7E5817417323453B CRC64;			

Query Match	79.6%;	Score 1253.5;	DB 11;	Length 283;
Best Local Similarity	87.3%;	Pred. No.3.1e-94;		
Matches 247;	Conservative 14;	Mismatches 21;	Indels 1;	Gaps 1
QY	28	MASLIGQIFWMSIISIIIIILAGAIALLIGFISGRHSITVTYVASAGNIGEDILSCTPEP	87	
Db	1	MASIGQIIFWMSITNTIIIIILAGAIALLIGFISGRKPIVTYTTTSAGNIGEDTILSCTPEP	60	
QY	88	DIKLSDIYIOMIKESVLGIYHFFKSGKDELSEODEMFRGRIVAPDQYIVGNASIRLKNV	147	
Db	61	DIKINGVIYQWLKEIKIGLVHFFKSGKDDLSCQHEMFRGRITVFADQYVVGASIRLKNV	120	
QY	148	QLTDAGTYKCYIITSGKGKNANLKYKTGAFSPDEVVNDVNASSETLRGCAEPPPOPTVY	207	
Db	121	QLTDAGTYCTYTRSSKKGKNALYKRTGAFSPDELINDVYNASSETLRCAEPPPOPTVY	180	
QY	208	MASQVDQGANFSEVSNISFELNSENVTMKVSVLYNTTNTYSQMIENDIKATGDIKY	267	
Db	181	MASQVDQGANFSEVSNISFELNSENVTMKVSVLYNTTNTYSQMIENDIKATGDIKY	240	
QY	268	TESRIKRRSHQLNLSKASLQV-SSEFALSWALLLSPTLMK	309	
Db	241	TDSEVKRRSQQLNLSGSPSPCVSSSAFVAGWALLLSLSCCLMR	283	

RESULT 6	
ID	Q7ZY30
AC	Q7ZY30
DT	01-JUN-2003 (TREMBLrel. 24, Created)
DT	01-JUN-2003 (TREMBLrel. 24, last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE	Hypothetical protein (Fragment).
OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC	Xenopodinae; Xenopus.
OX	NCBI_Taxid=8335;

[illegible]

QY	20	IRBEPBPAMASIQILFMBSIIIIIIILGALMIIIGPGLSRHSTLYTTVASAGNIEDG	73
Db	2	LRRSGSPGNG-----VHGALIGALMFCTGLALEVQPEDEPVVALVGDA	46
QY	80	ILSCTE--EBDIKLSDIVIOMLKEVGLVHREFEKGDLESHODEMERGRVAPADVIV	137
Db	47	TLCSSPSPEGFSLAQINLIWQTLTPKQVHSPFAGQD---QSSAVANRRALFPDLIAQ	1020
QY	138	GNASLILKNAVQLTDACTYCYIITTSKKGKNNLEKKTGA-FSMPEVNDVY----	ASSE 191
Db	103	GNASLILQRRVADDEGSLFCF-VSARDFPSAAVSLQVAAVAPSKPSMTLEPPKMDLRPGIV	167
QY	192	TLCCEAPRMVPOPTVYVAQVQAGNPFSEVSTSEFELSENVTMKVSVLVNVT-INNTY	250
Db	162	TTCSSYKRGPEAEVFM--QDQGGVPLTGNVYTS-QMNEGGLPDIYHSLAVLVGANGTY	218
QY	251	SCMIENDIAK--ATGDIKVT	268
Db	219	SCIVRNVPVLQODAHGSVIT	238

AC Q8NCB6; (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 25, last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE Hypothetical protein FLN90368.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxId=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Nakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
 RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.,
 RT "NEO human cDNA sequencing project."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK074849; BAC11243.1; -
 DR InterPro: IPR003599; Ig_1.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_4.
 DR SMART; SM00409; IGL1; 2.
 DR SMART; SM00408; IGL2; 4.
 DR SMART; SM00406; IGV; 2.
 DR PROSITE; PS00835; IG_LIKE; 4.
 KW Hypothetical protein; Immunoglobulin domain.
 SQ SEQUENCE 533 AA; 57179 MW; FCTE3E3A84F56A56 CRC64;

Query Match 15.6%; Score 246; DB 4; Length 533;
 Best Local Similarity 26.2%; Pred. No. 1.5e-11;
 Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

QY 19 QIRWESPAMASIGQ-----LF--WIIISIIIIILAGAILIGFGI---SGRIS 63
 DB 175 EVFWQGGQGVPLTGNVTTSSOMANEQGLFVHSLIRVLGANGSYSLVNRPNVLAQDAHSS 234
 QY 64 ITVTVAAS-----AGNIGEDGISCTP--EPDIKLSDIVIQWLKEGVLAGIV 107
 DB 235 VITTPQSPGTGAVEQVPEDPVALVGTDTATLRCSPPRPGSLAQLNIMQLTDTKQIV 294
 QY 108 HEFKGKDELSDQDEKFRGTAVFADQVTVGNASIRLKNVQLTDACTYKCYIITSKGN 167
 DB 295 HSFTEGRD---QGSAYANRTALFPDLAQGNASIRLQVRVADSGSFCTF-VSIRDFGS 349
 QY 168 ANLEYKTGA-FSMPEVNVN-----ASSETLRCEAPRFPQPTVYMASOVQGANFSEV 221
 DB 350 AAVSLQVAAPYKPSSTLEPNKDLRPGDVTITGSSYRGYPAEVFW--QDQGVPLTGN 407
 QY 222 SNTSELSNENVTMKVSVLYNVT-INNTYSCMIENDIAK--ATGDIKVT 268
 DB 408 VTTT-QMANEQGLFVHSLIRVLGANGSYSLVNRPNVLAQDAHSGVTT 456

RESULT 11

Q8NB18
 ID Q8NB18 PRELIMINARY; PRT; 534 AA.
 AC Q8NB18;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Hypothetical protein NT2RP3001861.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
 RA Saito K., Yamamoto J., Nakamatsu A., Nagai T., Nakamura Y.,
 RA Nagahari K., Sugano S., Isogai T.,
 RT "HRI human cDNA sequencing project."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK075549; BAC11692.1; -
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003598; Ig_c2.

DR InterPro: IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_4.
 DR SMART; SM00409; IGL1; 2.
 DR SMART; SM00407; IGL1; 2.
 DR SMART; SM00408; IGL2; 4.
 DR SMART; SM00406; IGV; 2.
 DR PROSITE; PS00835; IG_LIKE; 4.
 KW Hypothetical protein; Immunoglobulin domain.
 SQ SEQUENCE 534 AA; 57265 MW; 0FBIA65948417BBA CRC64;

Query Match 15.6%; Score 246; DB 4; Length 534;
 Best Local Similarity 26.2%; Pred. No. 1.5e-11;
 Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

QY 19 QIRWESPAMASIGQ-----LF--WIIISIIIIILAGAILIGFGI---SGRIS 63
 DB 175 EVFWQGGQGVPLTGNVTTSSOMANEQGLFVHSLIRVLGANGSYSLVNRPNVLAQDAHSS 234
 QY 64 ITVTVAAS-----AGNIGEDGISCTP--EPDIKLSDIVIQWLKEGVLAGIV 107
 DB 235 VITTPQSPGTGAVEQVPEDPVALVGTDTATLRCSPPRPGSLAQLNIMQLTDTKQIV 294
 QY 108 HEFKGKDELSDQDEKFRGTAVFADQVTVGNASIRLKNVQLTDACTYKCYIITSKGN 167
 DB 295 HSFTEGRD---QGSAYANRTALFPDLAQGNASIRLQVRVADSGSFCTF-VSIRDFGS 349
 QY 168 ANLEYKTGA-FSMPEVNVN-----ASSETLRCEAPRFPQPTVYMASOVQGANFSEV 221
 DB 350 AAVSLQVAAPYKPSSTLEPNKDLRPGDVTITGSSYRGYPAEVFW--QDQGVPLTGN 407
 QY 222 SNTSELSNENVTMKVSVLYNVT-INNTYSCMIENDIAK--ATGDIKVT 268
 DB 408 VTTT-QMANEQGLFVHSLIRVLGANGSYSLVNRPNVLAQDAHSGVTT 456

RESULT 12

Q8VE98
 ID Q8VE98 PRELIMINARY; PRT; 316 AA.
 AC Q8VE98;
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Similar to B7 homolog 3 (B7-H3).
 GN 603041IF23RIK OR AU016588 OR B7H3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.,
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Suh W.-K., Chung S., Bray M., Yoshinaga S.K.;
 RT "The B7 family member B7-H3 preferentially downregulates Th1-mediated
 immune responses."
 RL Nat. Immunol. 0:0-0(2003).
 DR EMBL; BC019436; AAH19436.1; -
 DR EMBL; AY190318; AAP04007.1; -
 DR MGD; MGI:2143194; 603041IF23RIK.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00409; IGL1; 2.
 DR PROSITE; PS00835; IG_LIKE; 2.
 SQ SEQUENCE 316 AA; 34001 MW; 7BA30B1E67F55827 CRC64;

Query Match 14.9%; Score 235; DB 11; Length 316;
 Best Local Similarity 27.7%; Pred. No. 5.6e-11;
 Matches 67; Conservative 46; Mismatches 111; Indels 18; Gaps 8;

QY 37 MSIIIIIIAGATALLIGFISGRHSITVTVAASAGNIGEDGILCTF--EPDIKLSDI 94
 Db 5 WGGPSVGVCMGTALG-VLCICLTGAVVQVSEDPVALVDTALRGSFSPSPGSLAQ 63
 QY 95 VIQWLKESVGLVHFEKPKDELSEODEMFRGTAFAVDQIVGNASIRLNQVLTAGT 154
 Db 64 NLIMQVLTDTKQVLSFTBGRD---QGSAYGNRTALFPDLIVQGNASIRLNQVLTAGT 119
 QY 155 YKCVIITSKSGKGNANLEKTAFAFMEPVNVN---ASSETLRCEAPRWFPOPTVMA 209
 Db 120 YTCFVSIOEDFSAVSIQVAAPYKSPWLTLEPNKDLRGNVTTTSSYGCPAEVFWK 179
 QY 210 SQVDQGANFSEVNSTFELNSENVTMKVSVLYNVT-INNTYSCMIENDIAK--ATGDIK 266
 Db 180 D--QGGVPLTGNVTTT--QMANERGLFDVHSLRVLANGNGYSLVNRNPNVLQDDAHGSVT 236
 QY 267 VT 268
 Db 237 IT 238

RESULT 13

Q7TPB4 PRELIMINARY; PRT; 316 AA.
 AC Q7TPB4;
 DT 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DB B7-H3.
 GN B7H3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sun W.-K., Chung S., Bray M., Yoshinaga S.K.;
 RT "The B7 family member B7-H3 preferentially downregulates Th1-mediated
 immune responses.";
 RL Nat. Immunol. 0:0-0(2003).
 DR EMBL: AY190319; AAF04008.1;
 SQ SEQUENCE 316 AA; 34074 MW; 80FB9D6BD0A4143B CRC64;

Query Match 14.7%; Score 232; DB 11; Length 316;
 Best Local Similarity 27.2%; Pred. No. 9.8e-11;
 Matches 66; Conservative 44; Mismatches 113; Indels 20; Gaps 8;

QY 37 MSIIIIIIAGATALLIGFISGRHSITVTVAASAGNIGEDGILCTF--EPDIKLSDI 94
 Db 5 WGGPSVGVCMGTALG-VLCICLTGAVVQVSEDPVALVDTALRGSFSPSPGSLAQ 63
 QY 95 VIQWLKESVGLVHFEKPKDELSEODEMFRGTAFAVDQIVGNASIRLNQVLTAGT 154
 Db 64 NLIMQVLTDTKQVLSFTBGRD---QGSAYGNRTALFPDLIVQGNASIRLNQVLTAGT 119
 QY 155 YKCVIITSKSGKGNANLEKTAFAFMEPVNVN---ASSETLRCEAPRWFPOPTVMA 209
 Db 120 YTCFVSIOEDFSAVSIQVAAPYKSPWLTLEPNKDLRGNVTTTSSYGCPAEVFWK 178
 QY 210 SQVDQGANFSEVNSTFELNSENVTMKVSVLYNVT-INNTYSCMIENDIAK--ATGDI 265
 Db 179 ---KGGGLPLTGNVTTTQMANERGLFDVHSLRVLANGNGYSLVNRNPNVLQDDAHGSV 235
 QY 266 KVT 268
 Db 236 TIT 238

RESULT 14
 Q9NM06 PRELIMINARY; PRT; 220 AA.
 AC Q9NM06;
 DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein FLJ20685.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ileal mucosa;
 RA Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,
 RA Hirao M., Ohmori Y., Ota T., Suzuki Y., Ohayashi M., Nishi T.,
 RA Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
 RT "MEDO human cDNA sequencing project.";
 RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK00692; BAA9123.1;
 DR InterPro: IPR003599; IG-
 DR InterPro: IPR007110; IG-like.
 DR Pfam: PF00047; IG_2
 DR SMART: SM00409; IG_1
 DR PROSITE: PS50835; IG-LIKE, 1.
 KW Hypothetical protein.
 SQ SEQUENCE 220 AA; 24979 MW; 66967620E130B515 CRC64;

Query Match 14.3%; Score 225; DB 4; Length 220;
 Best Local Similarity 31.1%; Pred. No. 2.2e-10;
 Matches 61; Conservative 32; Mismatches 81; Indels 22; Gaps 7;

QY 73 GNIGEDGILCTFEPDIKLSDIYIOWLKEGVLVHFEKPKDELSEODEMFRGTAFA 132
 Db 41 GRUDEDIILSPSE--RGSEVVIHWKYGQSY-KHVSYYGSHLESQDPRYANRISLFY 96
 QY 133 DQYIVGNASIRLNQVLTAGTGYKYIITSKSGKGNANLEKTAFAFMEPVNVN 192
 Db 97 NEIQNGNASLFFERVSILDEGIYTCYVGTAVITNKKVLYKAVVFLTPWKYKERNTSF 156
 QY 193 LRCEAPRWFPOPTVMA SQVDQGANFSEVNSTFELNSENVTMKVSVLYNVT-I 246
 Db 157 LICSUSLVYRPLIITM--KNDNTPISNNMEFISLDSFINSP-----LNTTGS 204
 QY 247 NNTYSCMIENDIAKAT 262
 Db 205 NSSYECTIENSILKQT 220

RESULT 15

Q9UM44 PRELIMINARY; PRT; 414 AA.
 AC Q9UM44;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DB HERV-H LTR associating protein 2 (HERV-H LTR-associating 2).
 GN HHLA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF126162; AAD48196.1;
 DR EMBL: BC035971; AAH35971.1;
 DR Genew; HGNC:4905; HHLA2.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 16:01:45 ; Search time 17 Seconds
(without alignments)
946.452 Million cell updates/sec

Title: US-09-827-271-392
Perfect score: 1574
Sequence: 1 HASAHASGRQRLHSASTQI.....SSFAISWALLPLSPYIMLK 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	215.5	13.7	526	1	BUTY_BOVIN
2	211.5	13.4	526	1	BUTY_HUMAN
3	178.5	11.3	524	1	BUTY_MOUSE
4	163.5	10.4	299	1	CD80_RABBIT
5	152	9.7	245	1	MOG_RAT
6	150.5	9.6	246	1	MOG_MOUSE
7	147.5	9.4	302	1	ICOL_HUMAN
8	147.5	9.4	329	1	CD86_HUMAN
9	147.5	9.4	330	1	CD86_RABBIT
10	144	9.1	247	1	MOG_HUMAN
11	143.5	9.1	309	1	CD86_MOUSE
12	140.5	8.9	246	1	MOG_BOVIN
13	135	8.6	761	1	NCA2_HUMAN
14	135	8.6	848	1	NCA1_HUMAN
15	134.5	8.5	503	1	SHS1_HUMAN
16	132.5	8.4	853	1	NCA1_BOVIN
17	131	8.3	1091	1	NCA1_CHICK
18	130.5	8.3	725	1	NCA2_MOUSE
19	130.5	8.3	1115	1	NCA1_MOUSE
20	128.5	8.2	858	1	NCA1_RAT
21	126.5	8.0	1088	1	NCA1_XENLA
22	125.5	8.0	298	1	JM42_HUMAN
23	124	7.9	306	1	CD80_MOUSE
24	123	7.8	365	1	CXAR_MOUSE
25	121	7.7	333	1	AMAL_DROME
26	121	7.7	1010	1	CONT_CHICK
27	120	7.6	215	1	CIR2_RAT
28	120	7.6	288	1	CD80_HUMAN
29	120	7.6	363	1	CXAR_HUMAN
30	119	7.6	325	1	DIM1_CAEEL
31	115.5	7.3	509	1	SHS1_RAT
32	115.5	7.3	1092	1	NCA2_XENLA
33	114.5	7.3	322	1	ICOL_MOUSE

34	113.5	7.2	1336	1	VGRI_RAT	P53767	rattus norv
35	113.5	7.2	1461	1	NEOI_HUMAN	O92559	homo sapien
36	113	7.2	359	1	LACH_DROME	Q24372	drosophila
37	112.5	7.1	337	1	OPCW_CHICK	Q98892	gallus gall
38	112.5	7.1	1018	1	CONT_HUMAN	Q12860	homo sapien
39	112.5	7.1	1020	1	CONT_MOUSE	P12960	homo sapien
40	110	7.0	1036	1	AXOI_CHICK	P26885	gallus gall
41	109.5	7.0	513	1	SHS1_MOUSE	P97797	m protein-t
42	109.5	7.0	1021	1	CONT_RAT	O63198	rattus norv
43	109.5	7.0	1377	1	NEOI_RAT	P97603	rattus norv
44	107.5	6.8	351	1	CD2_HUMAN	P06729	homo sapien
45	106.5	6.8	204	1	CTX2_HUMAN	Q96403	homo sapien

ALIGNMENTS

RESULT 1
ID BUTY_BOVIN STANDARD: PRT: 526 AA.
AC P18892: O18955; O18959;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Butyrophilin precursor (BT) (Butyrophilin subfamily 1 member A1).
GN BTN1A1 OR BTN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
RX MEDLINE=90354441; PubMed=2387867;
RA JACK L.V.W., Mather I.H.;
RT "Cloning and analysis of cDNA encoding bovine butyrophilin, an apical
RT glycoprotein expressed in mammary tissue and secreted in association
RT with the milk-fat globule membrane during lactation.";
RL J. Biol. Chem. 265:14481-14486(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein-Friesian;
RA Davey H.W., Ogg S.L., Husaini Y., Snell R.G., Korobko I.V.,
RA Mather I.H., Wilkins R.J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Seyfert H.-M., Luethen F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=95293916; PubMed=7775382;
RA Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.;
RT "Site-specific glycosylation of bovine butyrophilin.";
RL J. Biochem. 117:147-157(1995).
-!- FUNCTION: May function in the secretion of milk-fat droplets. It
may act as a specific membrane-associated receptor for the
association of cytoplasmic droplets with the apical plasma
membrane.
-!- SUBUNIT: Seems to associate with xanthine dehydrogenase/oxidase
(By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Expressed in mammary tissue and secreted in
association with the milk-fat-globule membrane during lactation.
-!- SIMILARITY: Belongs to the immunoglobulin superfamily. BTN/MOG
family.
-!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.

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DR EMBL; M35551; AAB39766.1; -
 DR EMBL; AF005497; AAB62889.1; -
 DR EMBL; Z93323; CAB07533.1; -
 DR PIR; A37821; A37821.
 DR InterPro; IPR001870; B302.
 DR InterPro; IPR007110; Ig_V.
 DR InterPro; IPR003596; Ig_V.
 DR InterPro; IPR006574; PRY.
 DR InterPro; IPR003877; SPRY_receptor.
 DR Pfam; PF00047; Ig_1.
 DR Pfam; PF00622; SPRY_1.
 DR SMART; SM00406; IgV_1.
 DR SMART; SM00589; PRY_1.
 DR SMART; SM00449; SPRY_1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal; Repeat.
 FT SIGNAL 1 26
 FT CHAIN 1 26
 FT DOMAIN 27 526
 FT TRANSMEM 27 526
 FT DOMAIN 243 269
 FT DOMAIN 270 526
 FT DOMAIN 27 140
 FT DOMAIN 148 234
 FT CARBOHYD 55 55
 FT CARBOHYD 215 215
 FT CONFLICT 35 35
 FT CONFLICT 230 230
 FT SEQUENCE 526 AA; 59276 MW; A14126802BD19284 CRC64;

Query Match 13.7%; Score 215.5; DB 1; Length 526;
 Best Local Similarity 24.5%; Pred. No. 1.3e-09;
 Matches 48; Conservative 49; Mismatches 94; Indels 5; Gaps 4;

QY 75 IGBDGLSTCFEPDILSDIVIQWLKEGVGLVHFEKGEKDELSEODEMFRGRTAVFAQD 134
 Db 42 VGDADALPRLSPNVAKGMELRFRKVPSPAVFVSGEGEGEAEYRGRVSLVEDH 101

QY 135 VIVGNASLRKLVQLTDACTYKCYIITSKGNANLEYTGAF-SMEVNVVDYNASSE-T 192
 Db 102 IAGSGVAVRIQEVASDDEGYRCFRODENYEELVHLKVALGSDPHISMVQESGEIC 161

QY 193 LRCEAPRPFOPPTVVAASQVDGANGSEVNSFELNSENVTKVYSVLYNTVINTTYSQ 252
 Db 162 LECTSVGMFPEPOVQ--RTHRGEEFSPNSERNPDEEG-LFTVAVSVIIRDSMKV-SC 218

QY 253 MIENDIAKATGDIKVT 268
 Db 219 CIRNLLIGKEKEVEVS 234

RESULT 2
 BUTY_HUMAN STANDARD; PRT; 526 AA.
 ID BUTY_HUMAN AC Q13410;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Butyrophilin precursor (BT) (Butyrophilin subfamily 1 member A1).
 GN BTNL1 OR BTN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast;
 RX MEDLINE=96201696; PubMed=8611614;
 RA Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.,
 RT "Cloning and sequence analysis of human butyrophilin reveals a

RT potential receptor function.",
 RL Biochim. Biophys. Acta 1306:1-4(1996).
 CC -!- FUNCTION: May function in the secretion of milk-fat droplets. It
 CC may act as a specific membrane-associated receptor for the
 CC association of cytoplasmic droplets with the apical plasma
 CC membrane (by similarity).
 CC -!- SUBUNIT: Seems to associate with xanthine dehydrogenase/oxidase
 CC (by similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. BTN/MOG
 CC family.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
 CC -----
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DR EMBL; U39576; AAC50489.1; -
 DR PIR; S70587; S70587.
 DR Genew; HGNC:1135; BTNL1.
 DR MIM; 601610; -
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR InterPro; IPR001870; B302.
 DR InterPro; IPR007110; Ig_V.
 DR InterPro; IPR003596; Ig_V.
 DR InterPro; IPR006574; PRY.
 DR InterPro; IPR003877; SPRY_receptor.
 DR Pfam; PF00047; Ig_1.
 DR Pfam; PF00622; SPRY_1.
 DR SMART; SM00406; IgV_1.
 DR SMART; SM00589; PRY_1.
 DR SMART; SM00449; SPRY_1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal; Repeat.
 FT SIGNAL 1 26
 FT CHAIN 1 26
 FT DOMAIN 27 526
 FT TRANSMEM 27 526
 FT TRANSMEM 243 269
 FT DOMAIN 270 526
 FT DOMAIN 27 140
 FT DOMAIN 148 234
 FT CARBOHYD 55 55
 FT CARBOHYD 215 215
 FT SEQUENCE 526 AA; 59004 MW; E9ECA0CF8DAF94D5 CRC64;

Query Match 13.4%; Score 211.5; DB 1; Length 526;
 Best Local Similarity 26.6%; Pred. No. 2.6e-09;
 Matches 49; Conservative 37; Mismatches 93; Indels 5; Gaps 4;

QY 75 IGBDGLSTCFEPDILSDIVIQWLKEGVGLVHFEKGEKDELSEODEMFRGRTAVFAQD 134
 Db 42 VGDADALPRLSPNVAKGMELRFRKVPSPAVFVSGEGEGEAEYRGRVSLVEDH 101

QY 135 VIVGNASLRKLVQLTDACTYKCYIITSKGNANLEYTGAF-SMEVNVVDYNASSE-T 192
 Db 102 IAGSGVAVRIQEVASDDEGYRCFRODENYEELVHLKVALGSDPHISMVQESGEIC 161

QY 193 LRCEAPRPFOPPTVVAASQVDGANGSEVNSFELNSENVTKVYSVLYNTVINTTYSQ 252
 Db 162 LECTSVGMFPEPOVQ--RTSKGEKFPSTSE-SRNPDEGLFTVAVSVIIRDTSTKRVSC 218

QY 253 MIEN 256
 Db 219 YIQN 222

RESULT 3
 BUTY_MOUSE

ID BUTY MOOSE STANDARD; PRT; 524 AA.
 AC Q62556; P97392;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Butyrophilin precursor (BT) (Butyrophilin subfamily 1 member A1).
 GN BTNL1 OR BTN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Mammary gland;
 RX MEDLINE=97148936; PubMed=8995761;
 RA Ogg S.L., Komaragiri M.V.S., Mather I.H.;
 RT "Structural organization and mammary-specific expression of the
 RT butyrophilin gene.";
 RL Mamm. Genome 7:900-905(1996).
 [2]
 RP SEQUENCE OF 39-487 FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=96125722; PubMed=8541302;
 RA Ishii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda T.;
 RT "Carboxy-terminal cytoplasmic domain of mouse butyrophilin
 RT specifically associates with a 150-kDa protein of mammary epithelial
 RT cells and milk fat globule membrane.";
 RL Biochim. Biophys. Acta 1245:285-292(1995).
 CC -1- FUNCTION: May function in the secretion of milk-fat droplets. It
 CC may act as a specific membrane-associated receptor for the
 CC association of cytoplasmic droplets with the apical plasma
 CC membrane (By similarity).
 CC -1- SUBUNIT: Seems to associate with xanthine dehydrogenase/oxidase.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in mammary tissue and secreted in
 CC association with the milk-fat globule membrane during lactation.
 CC -1- DEVELOPMENTAL STAGE: Expression increases during the last half of
 CC pregnancy and is maximal during lactation.
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. BTN/MOG
 CC family.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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 CC -----
 DR EMBL; U67065; AAB51034.1; -;
 DR EMBL; S80642; AAB35893.1; -;
 DR MGD; MGT;103118; Btntl1.
 DR InterPro: IPR001870; B302.
 DR InterPro: IPR007110; IG-V.
 DR InterPro: IPR003596; IG-V.
 DR InterPro: IPR006574; PRY.
 DR InterPro: IPR003877; SPRY_receptor.
 DR Pfam; PR00647; ig; 1.
 DR Pfam; PR00642; SPRY; 1.
 DR SMART; SM00406; IG; 1.
 DR SMART; SM00589; PRY; 1.
 DR SMART; SM00449; SPRY; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal; Repeat.
 FT SIGNAL 1 26
 FT CHAIN 27 524
 FT DOMAIN 27 247 BUTYROPHILIN.
 FT TRANSMEM 248 268 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 269 524 POTENTIAL.
 FT DOMAIN 29 141 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 149 235 IG-LIKE V-TYPE 1.
 FT CARBOHYD 56 56 IG-LIKE V-TYPE 2.
 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 46 46 D -> DD (IN REF. 2).
 FT CONFLICT 117 117 V -> F (IN REF. 2).
 FT CONFLICT 191 191 E -> D (IN REF. 2).
 FT CONFLICT 210 210 R -> S (IN REF. 2).
 FT CONFLICT 363 363 V -> E (IN REF. 2).
 FT CONFLICT 408 408 T -> K (IN REF. 2).
 FT CONFLICT 413 414 SL -> FF (IN REF. 2).
 FT CONFLICT 420 423 PRRV -> LAEY (IN REF. 2).
 FT CONFLICT 452 509 DIPSLPGLGGCTSGDKDT -> GHSLSVPAGRLYFWRQH
 FT (IN REF. 2).
 SQ SEQUENCE 524 AA; 58406 MW; 333f4DE2C7704480 CRC64;
 Query Match 11.3%; Score 178.5; DB 1; Length 524;
 Best Local Similarity 22.7%; Pred. No. 11e-06;
 Matches 45; Conservative 51; Mismatches 93; Indels 9; Gaps 4;
 QY 75 IGEDGILSTFEPDILKSDIVQWLKEGVLGVHEFEKEDBLSEQDEMRGRTRVAFADQ 134
 DB 43 VGSDAELTGFSPNASEYEMELMFRQTRSTAVLYLRDQDEGQCMTEYRGATLATAG 102
 QY 135 VVGNASLRLKXVQLTDACTYCYITTSKGNANLVEYTGAP-SMEVNVYNASSE-T 192
 DB 103 LLDGRATLIRIVRVSDQGEYRCLFKDNDFFEAAYLVKVAVSDPQISMTVQENGEME 162
 QY 193 LRCEAPRPMPPOPTVWASQVDGAFNSEVSNF--SPELNSEVNTKVVSVLVNTINNY 250
 DB 163 LECTSGMYEPQVQWRT-----GNREMPSTSESKHNEBGLFVAVASMTIRDSISKM 217
 QY 251 SCMIENDAKATGDIKVT 268
 DB 218 SCQIQNILLGQKREVIS 235
 RESULT 4
 CD80 RABIT STANDARD; PRT; 299 AA.
 ID CD80 RABIT
 AC P42070;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE T lymphocyte activation antigen CD80 precursor (Activation B7-1
 DE antigen).
 GN CD80.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B/J X CHB;HM;
 RX MEDLINE=95369849; PubMed=7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules.";
 RL Immunogenetics 42:217-220(1995).
 CC -1- FUNCTION: Involved in the costimulatory signal essential for T
 CC lymphocyte activation. T cell proliferation and cytokine
 CC production is induced by the binding of CD28 or CTLA-4 to this
 CC receptor.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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 CC -----
 DR EMBL; D49843; BAA08643.1; -;

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DR PIR: I46690; I46690.
DR HSSP, P33681, IDR9.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003599; Ig.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; Ig; 1.
DR PROSITE: PS50835; Ig-like; 2.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
  Receptor.
FT SIGNAL 1 32
FT CHAIN 33 299
FT DOMAIN 33 243
FT TRANSMEM 244 264
FT DOMAIN 265 299
FT DOMAIN 33 131
FT DOMAIN 144 225
FT DISULFID 49 115
FT CARBOHYD 161 215
FT CARBOHYD 52 52
FT CARBOHYD 88 88
FT CARBOHYD 97 97
FT CARBOHYD 122 122
FT CARBOHYD 185 185
FT CARBOHYD 206 206
FT CARBOHYD 210 210
SQ SEQUENCE 239 AA; 33513 MW; 67442235C91DE0 CRC64;

Query Match 10.4%; Score 163.5; DB 1; Length 299;
Best Local Similarity 25.3%; Pred. No. 8.3e-06;
Matches 73; Conservative 57; Mismatches 89; Indels 69; Gaps 19;

QY 40 ISIIIIAGATALLIGSGISGRHSITVTYVNASAGNIGDGLTCTFEDI-KLSDIYIOW 98
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  19 LCLTLALAG---LHPSGIS---QVTK---SVKEMALSCDYNISIDELARMRIYW 65
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 99 LKEG--VLGLVHEFEKDELSEODEMERGTAVFADQVIGVNASLRLKNVLDAGTYK 156
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  66 QKQDQWVLSIT---SQGVWPE---YKNT--FPD--IINISIMTLARLSDKGYIT 114
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 157 CYITTSKKGNANLEYKTA-----FSMEPV---NDVNASSETLRCAFPWFPQPT 205
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  115 C-VVQKEMGSPREHLSVTLSIRADFPVPSIDTIGHDPDENV--KIRCSASGSPBPR 171
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 206 VVNASOVDOGANFSEVSTFELNSENTMTAVSVL--YNTVNTYSCMIENDLAKXTGD 264
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  172 LAM---WEDGEELNAV-NTTVDQDLDTLTVSSSLDPNTNNNSIVCLIK-----YGE 221
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 265 IKVTE---SEIKRSHLQILNSKASLGVSSFFAISMALPLSPYLM 308
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  222 LSVSGIFPWSKPKQEPPIQLP-----FWIIVVSGALVL 256
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
MOG_RAT STANDARD; PRT; 245 AA.
ID MOG_RAT
AC Q63345;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin-oligodendrocyte glycoprotein precursor.
GN MOG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=93085763; PubMed=1453482;
RA Gardiner M.V., Amiguet P., Lington C., Mathieu J.-M.;
RT "Myelin/oligodendrocyte glycoprotein is a unique member of the
  immunoglobulin superfamily."
RL J. Neurosci. Res. 33:177-187(1992).
RN [2]

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RP SEQUENCE OF 28-245 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93376728; PubMed=8367453;
RA Pham-Dinh D., Matrie M.-G., Nusbaum J.-L., Rousset G.,
RA Pontarotti P., Roedel N., Mather I.H., Attiz K., Lindahl K.F.,
RA Dautigny A.;
RT "Myelin/oligodendrocyte glycoprotein is a member of a subset of the
  immunoglobulin superfamily encoded within the major
  histocompatibility complex."
RT Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
RN [3]
RP STRUCTURE BY NMR OF 62-82.
RX MEDLINE=97354172; PubMed=9210466;
RA Albouze-Abou S., Wilson J.C., Bernard C.C.A., von Itzstein M.;
RT "A conformational study of the human and rat encephalitogenic myelin
  oligodendrocyte glycoprotein peptides 35-55."
RL Eur. J. Biochem. 246:59-70(1997).
CC -1- FUNCTION: Minor component of the myelin sheath. May be involved in
  completion and/or maintenance of the myelin sheath and in cell-
  cell communication.
CC -1- SUBUNIT: May form homodimers.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Found exclusively in the CNS, where it is
  localized on the surface of myelin and oligodendrocyte cytoplasmic
  membranes.
CC -1- DEVELOPMENTAL STAGE: A PEAK OF EXPRESSION HAS BEEN OBSERVED
  BETWEEN POSTNATAL DAYS 15 AND 25, COINCIDENT WITH THE PERIOD OF
  ACTIVE MYELINATION.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. BTN/MOG
  family.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- CAUTION: Do not confuse myelin-oligodendrocyte glycoprotein (MOG)
  with oligodendrocyte-myelin glycoprotein (OMG).
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  or send an email to license@isb-sib.ch).
CC
DR EMBL: M99485; AAA4628.1; -
DR EMBL: L21995; AAF74786.1; -
DR PIR: B47712; B47712.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS50835; Ig-like; 1.
KW Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.
FT SIGNAL 1 27
FT CHAIN 28 245
FT DOMAIN 28 155
FT TRANSMEM 156 176
FT DOMAIN 177 208
FT TRANSMEM 209 229
FT DOMAIN 230 245
FT DOMAIN 30 139
FT DISULFID 51 125
FT CARBOHYD 58 58
SQ SEQUENCE 245 AA; 27881 MW; C97F8AD60DA32B4 CRC64;

Query Match 9.7%; Score 152; DB 1; Length 245;
Best Local Similarity 26.2%; Pred. No. 5.3e-05;
Matches 39; Conservative 31; Mismatches 55; Indels 24; Gaps 5;

QY 37 WS-----ISIIII-----AGATALLIGSGISGRHSITVTYVNASAGNIGDGLTCT 84
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  5 WSLSLPSGLSLILLIQLQLSRYTAGQPR-VLPG---HPIRAL-----VSGEALPGR 52
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 85 FEPDIKLSDIVIQWLKEGVLGLVHEFEKDELSEODEMERGTAVFADQVIGVNASLRL 144
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 53 ISPGKNAATGMEVGMKSPRSRVVHLNRNGKDQDAEQAPRYGRTELLKESIGKVALRI 112
 QY 145 KAVOLTDAITYKYCIITSGKGNANLEYK 173
 Db 113 QNVRFSDEGTYCTCFPRDHSYQEBAAVELK 141

RESULT 6
 MOG_MOUSE STANDARD; PRT; 246 AA.
 AC 061865; P70364; Q62003;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Myelin-oligodendrocyte glycoprotein precursor.
 GN MOS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=95130110; PubMed=7829100;
 RA Dautigny A.; Pham-Dinh D.; Dautigny A.;
 RT "Structure and polymorphism of the mouse myelin/oligodendrocyte
 RT glycoprotein gene."
 RL Genomics 23:36-41(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Gardiner M.V.; Mathieu J.M.;
 RT "Murine and human MOG are highly conserved: cDNA analysis."
 RL Trans. Am. Soc. Neurochem. 24:234-234(1993).
 RN [3]
 RP SEQUENCE OF 29-246 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=93376728; PubMed=8367453;
 RA Pham-Dinh D.; Mattei M.-G.; Nussbaum J.-L.; Roussel G.;
 RA Pontarotti P.; Roessel N.; Mather I.H.; Artzt K.; Lindahl K.F.;
 RA Dautigny A.;
 RT "Myelin/oligodendrocyte glycoprotein is a member of a subset of the
 RT immunoglobulin superfamily encoded within the major
 RT histocompatibility complex."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
 RN [4]
 RP SEQUENCE OF 29-54.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=92218912; PubMed=1373175;
 RA Amiguet P.; Gardiner M.V.; Zanetta J.-P.; Mathieu J.-M.;
 RT "Purification and partial structural and functional characterization
 RT of mouse myelin/oligodendrocyte glycoprotein."
 RL J. Neurochem. 58:1676-1682(1992).
 CC -1- FUNCTION: Minor component of the myelin sheath. May be involved in
 CC completion and/or maintenance of the myelin sheath and in cell-
 CC cell communication.
 CC -1- SUBUNIT: May form homodimers.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Found exclusively in the CNS, where it is
 CC localized on the surface of myelin and oligodendrocyte cytoplasmic
 CC membranes.
 CC -1- DISEASE: Reduced concentrations of MOG are observed in jimpy and
 CC quacking dysmyelinating mutant mice.
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. EFN/MOG
 CC family.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- CAUTION: Do not confuse myelin-oligodendrocyte glycoprotein (MOG)
 CC with oligodendrocyte-myelin glycoprotein (OMG).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; L29503; AAC42023.1; -
 CC DR EMBL; L29498; AAC42023.1; JOINED.
 CC DR EMBL; L29500; AAC42023.1; JOINED.
 CC DR EMBL; L29501; AAC42023.1; JOINED.
 CC DR EMBL; L29499; AAC42023.1; JOINED.
 CC DR EMBL; L29502; AAC42023.1; JOINED.
 CC DR EMBL; U64572; AAB08096.1; -
 CC DR EMBL; L20942; AAB03180.1; -
 CC DR PIR; A55717; A55717.
 CC DR MGD; MGI:97435; MOG.
 CC DR InterPro; IPR007110; Ig-like.
 CC DR InterPro; IPR003596; Ig-like.
 CC DR Pfam; PF00047; Ig_1.
 CC DR SMART; SM00406; IGV; 1.
 CC DR PROSITE; PS50835; IG LIKE.
 CC KW Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.
 CC FT SIGNAL 1 28
 CC FT CHAIN 29 246 MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.
 CC FT DOMAIN 29 156 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 157 177 POTENTIAL.
 CC FT DOMAIN 178 209 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 210 230 POTENTIAL.
 CC FT DOMAIN 231 246 EXTRACELLULAR (POTENTIAL).
 CC FT DOMAIN 31 144 IG-LIKE V-TYPE.
 CC FT DISULFID 52 126 POTENTIAL.
 CC FT CARBOHYD 59 59 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CONFLICT 21 21 L -> IL (IN REF. 2).
 CC FT CONFLICT 32 32 R -> G (IN REF. 4).
 CC FT CONFLICT 95 95 G -> E (IN REF. 3).
 CC FT CONFLICT 169 169 P -> S (IN REF. 2).
 CC SQ SEQUENCE 246 AA; 28271 MW; 1FLA8A4AD05CFB89 CRC64;

Query Match 9.6%; Score 150.5; DB 1; Length 246;
 Best Local Similarity 23.8%; Pred. No. 7e-05;
 Matches 34; Conservative 33; Mismatches 65; Indels 11; Gaps 2;

QY 37 WS-----ISITIIILAGAIILITGFGISGRHSITVTVAAGNIGEDGISCTEPPDIK 90
 Db 5 WSFWSWPSCHFLDLTL-----LQLSCSYAGQFRVIGPGIPALVGDFAELPCRSFGKN 59
 QY 91 LSDIVIOGLKGVGLVHEFEKGDSEODMEHGRTAFFDQYIVGASIRLNKVOIT 150
 Db 60 ATGWEVGMKSPRSRVVHLNRNGKDQDAEQAPRYGRTELLKETSBGKVTLRIONVRS 119
 QY 151 DAGTYKYCIITSGKGNANLEYK 173
 Db 120 DEGYTCTCFPRDHSYQEBAAVELK 142

RESULT 7
 ICOL_HUMAN STANDARD; PRT; 302 AA.
 AC 075144; Q9HDI8; Q9HDI8; Q9HDI8;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein G150)
 DE (B7-related precursor (B7 homolog 1) (B7RP-1).
 GN ICOSL OR B7H2 OR B7RP1 OR KIAA0653.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Dendritic cell;
 RX MEDLINE=20477846; PubMed=11023515;
 RA Wang S.; Zhu G.; Chapoval A.I.; Dong H.; Tamada K.; Ni J.; Chen L.;
 RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds
 RT ICOS.";

RL Blood 96:2808-2813(2000).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.

RC TISSUE-Peripheral blood lymphocytes;

RX MEDLINE=20465019; PubMed=11007762;

RA Yoshinaga S.K., Zhang M., Picotillo J., Horan T., Khare S.D., Miner K., Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H., Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;

RT "Characterization of a new human B7-related protein: B7RP-1 is the ligand to the co-stimulatory protein ICOS.";

RL Int. Immunol. 12:1439-1447(2000).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Leukocyte;

RX MEDLINE=20126021; PubMed=10657606;

RA Ling V., Wu P.W., Finerly H.F., Bean K.M., Spaulding V., Fouser L.A., Leonard J.P., Hunter S.E., Zoller R., Thomas J.U., Miyashiro J.S., Jacobs K.A., Collins M.;

RT "Identification of GL50, a novel B7-like protein that functionally binds to ICOS receptor.";

RL J. Immunol. 164:1653-1657(2000).

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

RL DNA Res. 5:169-176(1998).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RA Ling V., Dunne J., Danneberg J., Danneberg J. K.;

RT "GL50 molecules and uses thereof.";

RL Patent number WO0121796, 29-MAR-2001.

CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoform=2;

CC Comment=Additional isoforms seem to exist;

CC Name=1;

CC IsoId=O75144-1; Sequence=Displayed;

CC Name=2;

CC IsoId=O75144-2; Sequence=VSP_002520;

CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART, KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES, SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN LYMPH NODES, LEUKOCYTES AND SPLEEN.

CC -1- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.

CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. BTN/MOS family.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -1- CAUTION: Ref.4 sequence differs from that shown in position 300 onward for an unknown reason.

CC -----

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CC -----

DR EMBL: AF199028; AAF34739.1; -

DR EMBL: AF289028; AAG01176.1; -

DR EMBL: AF216749; AAK16241.1; -

DR EMBL: AB014553; BAA31628.1; ALT SEQ.

DR EMBL: AX100599; CAC36465.1; -

DR MIM: 605717; -

DR GO: GO:0016021; C:integral to membrane; NAS.

DR GO: GO:0003793; F:defense/immunity protein activity; NAS.

DR GO: GO:0005102; F:receptor binding; TAS.

DR GO: GO:0042104; P:positive regulation of activated T-cell pro. .; TAS.

DR GO: GO:0007165; P:signal transduction; NAS.

DR GO: GO:0042110; P:T-cell activation; NAS.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003599; IG.

DR Pfam: PF00047; Ig_2.

DR SMART: SM00409; Ig_1.

DR PROSITE: PS00835; IG_LIKE_2.

DR K: B-cell activation; Immune response; Glycoprotein;

KW Immunoglobulin domain; Signal; Transmembrane; Multigene family;

KW Alternative splicing.

FT SIGNAL 1 18

FT CHAIN 19 302

FT DOMAIN 19 256

FT TRANSMEM 257 277

FT DOMAIN 278 302

FT DOMAIN 19 129

FT DOMAIN 141 227

FT DISULFID 37 113

FT DISULFID 158 216

FT CARBOHYD 70 70

FT CARBOHYD 137 137

FT CARBOHYD 173 173

FT CARBOHYD 166 186

FT CARBOHYD 225 225

FT VARSPLIC 300 302

FT FTId=VSP_002520.

SEQ SEQUENCE 302 AA; 33349 MW; 647934E21B55E34A CRC64;

Query Match 9.4%; Score 147.5; DB 1; Length 302;

Best Local Similarity 24.5%; Pred. No. 0.000167;

Matches 66; Conservative 41; Mismatches 117; Indels 45; Gaps 13;

QY 75 IGEDGILCTFEPD--IKLSDIVIQWLKEGVGLVHEKEGKDELSEDEMFGRTAYV 131

DB 29 VGSDELSCAC-PEGRFPLNDVYVWQSEKTVTYHLPQSSLENDSDRRNALMS 87

QY 132 ADQVIVGNASLRKLVQTDAGTYKCYITTSKGG-----NANLEKTKGA-PSMEPVND 185

DB 88 PAGMLRGDSLRFLFVTLPDDEQKFC-LVLSQSLGFQEVLSYEVLHVANFSVPVVSAP 146

QY 186 YNASSS--TLRCAPRPFPQPVVNASQVDQGANFSEVNTSPELNSEVTKKVSVLVN 243

DB 147 HESQDELFTCTGINSYRPNVYWKNTDNLDOALQNDVFLNMRGL-YDVSVLRI 205

QY 244 V-TINNTYSCMIEN-----DIATYG-DI-----KVTESEI---KRSHPQLNSKAS 286

DB 206 ARPVSNICCIENVLQONLTVGSQTGNDIGRDKITENPVSTGSKNATWISLAVLC 265

QY 287 L-----CVSSFPALSWALLP 301

DB 266 LVVAVAVAGVCRDRCLQHSYAGAMAVSP 294

RESULT 8

ID CD86_HUMAN STANDARD; PRT; 329 AA.

AC P42081; Q13655;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE T lymphocyte activation antigen CD86 precursor (Activation B7-2 antigen) (CTLA-4 counter-receptor B7.2) (B70) (BUN-1) (BUE3).

GN CD86 OR CD28LG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94053735; PubMed=7694363;
 RA Freeman G.J., Gribben J.G., Boussiotis V.A., Ng J.W.,
 RA Restivo V.A., Jr., Lombard L.A., Gray G.S., Nadler L.M.,
 RT "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T
 RT cell proliferation.";
 RL Science 262:903-911 (1993).
 RN [2]
 RP SEQUENCE OF 7-329 FROM N.A.
 RX MEDLINE=94050123; PubMed=7694153;
 RA Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,
 RA Lanier L.L., Somoza C.,
 RT "B70 antigen is a second ligand for CTLA-4 and CD28.";
 RL Nature 366:76-79 (1993).
 RN [3]
 RP SEQUENCE OF 7-329 FROM N.A.
 RX TISSUE=Forebrain;
 MEDLINE=9531831; PubMed=7541777;
 RA Jellis C.L., Wang S.S., Rennett P., Borriello F., Sharpe A.H.,
 RA Green N.R., Gray G.S.,
 RT "Genomic organization of the gene coding for the costimulatory human
 RT B-lymphocyte antigen B7-2 (CD86)."
 RL Immunogenetics 42:85-89 (1995).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=95088403; PubMed=7527824;
 RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
 RA Okumura K., Ito D., Azuma M.,
 RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
 RT cell proliferation, cytokine production, and generation of CTL.";
 RL J. Immunol. 154:97-105 (1995).
 RN [5]
 RP IDENTIFICATION AS CD86.
 RX MEDLINE=94348060; PubMed=7520767;
 RA Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,
 RA Nadler L.M., Wakasa H., Tedder T.F.,
 RT "The B7-2 (B70) costimulatory molecule expressed by monocytes and
 RT activated B lymphocytes is the CD86 differentiation antigen.";
 RL Blood 84:1402-1407 (1994).
 RN [6]
 RP FUNCTION: Receptor involved in the costimulatory signal essential
 CC for T lymphocyte proliferation and interleukin 2 production, by
 CC binding CD28 or CTLA-4. May play a critical role in the early
 CC events of T cell activation and costimulation of naive T cells,
 CC such as deciding between immunity and anergy that is made by T
 CC cells within 24 hours after activation.
 CC [7]
 RP SUBCELLULAR LOCATION: Type I membrane protein.
 CC [8]
 RP TISSUE SPECIFICITY: Expressed by activated B lymphocytes and
 CC monocytes.
 CC [9]
 RP SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC [10]
 RP SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC [11]
 RP DATABASE: NAME=PROT; NOTE=CD guide CD86 entry;
 CC WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd86.htm".
 CC [12]
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 CC or send an email to license@isb-sib.ch).
 CC [13]
 RP EMBL: L25259; AAAS8389.1; -
 DR EMBL: U04343; AAB03814.1; -
 DR EMBL: U17722; AAB6473.1; -
 DR EMBL: U17717; AAA86473.1; JOINED.
 DR EMBL: U17718; AAA86473.1; JOINED.
 DR EMBL: U17719; AAA86473.1; JOINED.

DR EMBL: U17721; AAA86473.1; JOINED.
 DR PIR: A48754; A48754.
 DR PDB: 1185; 04-APR-01.
 DR Genew; HGNC:1705; CD86.
 DR MIM: 601020; -
 DR GO: GO:0004872; P:receptor activity; TAS.
 DR GO: GO:0006955; P:immune response; TAS.
 DR GO: GO:0008284; P:positive regulation of cell proliferation; TAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003006; Ig_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00290; IG_LIKE; 1.
 DR PROSITE: PS00290; IG_MHC; FALSE NEG.
 DR Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor; Polymorphism; 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 329
 FT DOMAIN 24 247
 FT TRANSMEM 248 268
 FT DOMAIN 269 329
 FT DOMAIN 33 131
 FT DOMAIN 150 225
 FT DISULFID 40 110
 FT CARBOHYD 157 218
 FT CARBOHYD 33 33
 FT CARBOHYD 47 47
 FT CARBOHYD 135 135
 FT CARBOHYD 146 146
 FT CARBOHYD 154 154
 FT CARBOHYD 177 177
 FT CARBOHYD 192 192
 FT CARBOHYD 213 213
 FT VARIANT 310
 FT A->T (in dbSNP:1129055).
 FT /FTID=VAR 014650.
 FT K->E (IN REF. 3).
 FT CONFLICT 27 27
 FT SEQ 329 AA; 37696 MW; 65D4F3826889CF7D CRC64;
 SQ
 Query Match 9.4%; Score 147.5; DB 1; Length 329;
 Best Local Similarity 23.4%; Pred. No. 0.00018;
 Matches 67; Conservative 43; Mismatches 109; Indels 67; Gaps 13;
 QY 50 IALLIFGSGISGRHSIVTTVAAGNIGDGIISCTP--PPDIKLSIVIOWLKEVLYGV 107
 DB 12 ILFVAFLLSGAAPLKIQAY-----PNIADLPCCQANQNSLSLVVFMQDENT-VI 65
 QY 108 HEFKSGKDELSEODEMFRGRTAVPADQVIVGNASIRLKNVOLTDACTYKCYIITSKGG- 166
 DB 66 NEVYLKKEKFPDSVHSKYMGRTEFSDS-----SWTLRLHNLQIKDKGLYOCIIHKKRPTGM 120
 QY 167 ----NANLEPKYGA-FSMREV-----NVDYNASSELRCAAPRMFRPPTVMAQVVDGAGN 217
 DB 121 IRIHQNSELSTLVANSOPEIVISNITENVYI-NLTGSHHGYP----- 166
 QY 218 FSEVNSTSEFLNSENVTKV-----VSVLNVNTI-----NNTYSQMIEN 256
 DB 167 ----KKGVSLTLTKNSTIYDGMQSGQNVHLYVSLSSVSPDVSNNMIFCILET 222
 QY 257 DIAKATGDIKVTSEIKR--RSHLOQLNS--KASICVSGSFPALISW 297
 DB 223 DKTRLLSPFSIELEDDPPDPDHPITVLPVLIICVAVFCILIW 268
 RESULT 9
 ID CD86_RABIT STANDARD; PRT; 330 AA.
 AC P42071;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE B lymphocyte activation antigen CD86 precursor (Activation B7-2
 GN antigen).
 GN CD86.

```

OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B/J X CHB;HM;
RX MEDLINE=95369849; PubMed=7642234;
RA Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
RT costimulatory molecules."
RL Immunogenetics 42:217-220(1995).
CC -1- FUNCTION: Receptor involved in the costimulatory signal essential
CC for T lymphocyte proliferation and interleukin 2 production, by
CC binding CD28 or CTLA-4. May play a critical role in the early
CC events of T cell activation and costimulation of naive T cells,
CC such as deciding between immunity and anergy that is made by T
CC cells within 24 hours after activation.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-----
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DR EMBL; D49842; BAA08642.1; -.
DR PIR; I46691; I46691.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003106; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
DR PROSITE; PSS00290; IG MHC; 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL 1 22
FT CHAIN 23 330
FT DOMAIN 23 247
FT TRANSMEM 248 268
FT DOMAIN 269 330
FT DOMAIN 33 127
FT DOMAIN 150 225
FT DISULFID 40 110
FT DISULFID 157 218
FT CARBOHYD 33 33
FT CARBOHYD 135 135
FT CARBOHYD 146 146
FT CARBOHYD 154 154
FT CARBOHYD 177 177
FT CARBOHYD 192 192
FT CARBOHYD 198 198
FT CARBOHYD 213 213
SQ SEQUENCE 330 AA; 37142 MW; 935CDD65C57B3EB1 CRC64;

Query Match 9.4%; Score 147.5; DB 1; Length 330;
Best Local Similarity 24.0%; Pred. No. 0.00018;
Matches 59; Conservative 44; Mismatches 80; Indels 63; Gaps 11;

QY 38 SIISIIILGALILIGFISGRHSITVTVASAGNIGSDGLISCTF--EPDIKLSDIY 95
Db 12 TTFVMAIISGASIRI-----QAFNKTADLPQCFNLSQSRSLSEIV 54

QY 96 IQWLKSGVGLVHFPEKQDELSEBQDMFERKRAVFAADQYIVGNASIRLNKVLDTAGTY 155
Db 55 VFQODERL-VLYELFGRKRPNVDPKTYGRSTF--DQ---ESWNIQLNVAIKDKGVY 108

QY 156 KCVIISKKGK-----NANLEYKGA-FSMPEVNVVDNA---SSETILCAAPKWPFPQPTV 206

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Db 109 QCFVHHGAKGLVPIYQMSSELVLNFTQPEITLISNTRNSAINLTCSSVGYPEPK 168
QY 207 VMA5QVDQANPSEVNSNTEFELNSENVTKV-----VSVLVNTINNTYSCMIEN 256
Db 169 MF-----FVLKTEVATTEYGVIEKSDQDNTVGLKNISISG--STFSF 209

QY 257 DIAKAT 262
Db 210 DIRNAT 215

RESULT 10
MOG HUMAN
ID MOG HUMAN STANDARD; PRT; 247 AA.
AC Q16653; Q00713; Q00714; Q00715; Q13054; Q13055; Q14855; Q92891;
AC Q92892; Q92893; Q92894; Q92895; Q93053; Q96K09; Q96K09; Q96K05;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin-oligodendrocyte glycoprotein precursor.
GN MOG.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=95310943; PubMed=7790876;
RA Hilton A.A., Slavin A.J., Hilton D.J., Bernard C.C.A.;
RT "Characterization of cDNA and genomic clones encoding human myelin
RT oligodendrocyte glycoprotein."
RL J. Neurochem. 65:309-318(1995).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95054056; PubMed=7964757;
RA Pham-Dinh D., Alliquant B., Ruberg M., della Gaspera B.,
RA Nussbaum J.-L., Dautigny A.;
RT "Characterization and expression of the cDNA coding for the human
RT myelin/oligodendrocyte glycoprotein."
RL J. Neurochem. 63:2353-2356(1994).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96015053; PubMed=8530032;
RA Roth M.-P., Malfroy L., Offer C., Sevin J., Enault G., Borot N.,
RA Pontarotti P., Coppin H.;
RT "The human myelin oligodendrocyte glycoprotein (MOG) gene: complete
RT nucleotide sequence and structural characterization."
RL Genomics 28:241-250(1995).
[4]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=96115584; PubMed=8666381;
RA Pham-Dinh D., della Gaspera B., de Rosbo N.K., Dautigny A.;
RT "Structure of the human myelin/oligodendrocyte glycoprotein gene and
RT multiple alternative spliced isoforms."
RL Genomics 29:345-352(1995).
[5]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RA Ballenthin P.A., Gardiner M.V.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A. (ISOFORMS 1, 5 AND 7).
RA Griffiths C.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
[7]
RP STRUCTURE BY NMR OF 64-84.
RX MEDLINE=97354172; PubMed=9210466;
RA Alboz-Bo S., Wilson J.C., Bernard C.C.A., von Itzstein M.;
RT "A conformational study of the human and rat encephalitogenic myelin
RT oligodendrocyte glycoprotein peptides 35-55."
RL Eur. J. Biochem. 246:59-70(1997).
-1- FUNCTION: Minor component of the myelin sheath. May be involved in
completion and/or maintenance of the myelin sheath and in cell-

```


RT T cell proliferation and interleukin 2 production.";
 RL J. Exp. Med. 178:2185-2192(1993).
 RN [2]
 RC SEQUENCE FROM N.A.
 RK STRAIN-129; PubMed=7499829;
 RA MEDLINE=96094437; PubMed=7499829;
 RT Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;
 RL "Differential expression of alternate MB7-2 transcripts.";
 J. Immunol. 155:5490-5497(1995).
 [3]
 RP SEQUENCE OF 7-309 FROM N.A.
 RA MEDLINE=94230971; PubMed=7513726;
 RX Chen C., Gault A., Shen L., Nabavi N.;
 RT "Molecular cloning and expression of early T cell costimulatory
 RT molecule-1 and its characterization as B7-2 molecule.";
 RL J. Immunol. 152:4929-4936(1994).
 CC -1- FUNCTION: Receptor involved in the costimulatory signal essential
 CC for T lymphocyte proliferation and interleukin 2 production, by
 CC binding CD28 or CTLA-4. May play a critical role in the early
 CC events of T cell activation and costimulation of naive T cells,
 CC such as deciding between immunity and anergy that is made by T
 CC cells within 24 hours after activation.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed on activated B cells.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-7 is the initiator.
 CC
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FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 309 AA; 34665 MW; 8F58DC1F8B1D5EA CRC64;
 Query Match 9.1%; Score 143.5; DB 1; Length 309;
 Best Local Similarity 22.6%; Pred. No. 0.00034;
 Matches 50; Conservative 53; Mismatches 83; Indels 35; Gaps 10;
 QY 64 ITVTYVASKNT-----GEDGLSCFP--EPDIKLSDIYQWLKGVLYVHFYKGD 115
 Db 15 VYLLISDVSVETQAVFNGTAVLPFPFYKAQNISSEIVEFWQDOOL-VLYEHYLGTE 73
 QY 116 ELSEODEMRGRVAVADQVTVGNASRLKNVQLTQAGTYKCYIISKGNANLEYK-- 173
 Db 74 KLDVNAKILGRISF--DR--NNWTLRLHNVQIKOMGSYDGRFKKPPGSIILQOQLT 128
 QY 174 ---TGAFSMEPVYNDVNASSET--LRCEAPRFPQPTVWVASQVDGANGFSEVENTSP 226
 Db 129 ELSVIANFSEPEIKLAQNTGNSGINTCTSKQGHKPKMYPLINTSTVEGD---NM 184
 QY 227 ELSENVTMKVSVLYNVIT-----NNTYSMTINDIAK 260
 Db 185 QISQDNVT-ELFSISNSISLSPFDGVMHTVVCLETESMK 224
 RESULT 12
 ID_MOG_BOVIN STANDARD; PRT; 246 AA.
 AC P55803;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Myelin-oligodendrocyte glycoprotein precursor.
 GN MOG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 63-70.
 RC TISSUE=Brain;
 RX MEDLINE=93376728; PubMed=8367453;
 RA Pham-Dinh D., Mattei M.-G., Nussbaum J.-L., Rousset G.,
 RA Pontarotti P., Roedel N., Mather I.H., Artzt K., Lindahl K.F.,
 RA Dautigny A.;
 RT "Myelin/oligodendrocyte glycoprotein is a member of a subset of the
 RT immunoglobulin superfamily encoded within the major
 RT histocompatibility complex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
 [2]
 RP SEQUENCE OF 29-36.
 RC TISSUE=Brain;
 RX MEDLINE=93382604; PubMed=8371836;
 RA Birling M.C., Rousset G., Nussbaum J.-L.,
 RA "Biochemical and immunohistochemical studies with specific polyclonal
 RT antibodies directed against bovine myelin/oligodendrocyte
 RT glycoprotein.";
 RL Neurochem. Res. 18:937-945(1993).
 CC -1- FUNCTION: Minor component of the myelin sheath. May be involved in
 CC completion and/or maintenance of the myelin sheath and in cell-
 CC cell communication.
 CC -1- SUBUNIT: May form homodimers.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Found exclusively in the CNS, where it is
 CC localized on the surface of myelin and oligodendrocyte cytoplasmic
 CC membranes.

CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. BTN/MOG family.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- CAUTION: Do not confuse myelin-oligodendrocyte glycoprotein (MOG) with oligodendrocyte-myelin glycoprotein (OMG).
 CC -----
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 CC -----
 CC EMBL: L21757; -; NOT_ANNOTATED_CDS.
 CC PIR: A47712; A47712.
 CC HSSP: Q13740; 1KIC.
 CC InterPro: IPR007110; Ig-like.
 CC InterPro: IPR003596; Ig_v.
 CC Pfam: PF00047; Ig_v.
 CC SMART: SM00406; Ig_v; 1.
 CC PROSITE: PS50835; Ig_Like; 1.
 CC Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.
 KM SIGNAL 1 28
 FT CHAIN 1 28
 FT DOMAIN 29 246
 FT TRANSMEM 29 153
 FT DOMAIN 154 174
 FT TRANSMEM 175 209
 FT DOMAIN 210 230
 FT DOMAIN 231 246
 FT DOMAIN 29 144
 FT DISULFID 52 126
 FT CARBOHYD 59 59
 SQ SEQUENCE 246 AA; 28028 MW; 363C76A1A33BD41 CRG64; (POTENTIAL).
 Query Match 8.9%; Score 140.5; DB 1; Length 246;
 Best Local Similarity 26.1%; Pred. No. 0.00044;
 Matches 31; Conservative 25; Mismatches 50; Indels 13; Gaps 1;
 QY 68 TVASAGN-----IGEDGILSCFFEDIKSLDIIVQWLKGVLGIVHEKKEK 114
 DB 24 TSSSAGQFRVIGGHRIRLAVGDEVLPRISBGNKATGEMWYPPRSRVHLTRNCK 83
 QY 115 DELSEQDEMFRGTAVFADQVIVGNASLRKLVQLTADGYKCYITTSKGNANLEK 173
 DB 84 DDDEQAPRYRGRTQLKKEITIGSKVTLIRNVRFSDGGFTCFPFDSHYQEBAAWEK 142
 RESULT 13
 NCAM2_HUMAN STANDARD; PRT; 761 AA.
 AC P13592; P13593;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neural cell adhesion molecule 1, 120 kDa isoform precursor (N-CAM 120)
 DE (NCAM-120) (CD56 antigen).
 GN NCAM1 OR NCAM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A. (ISOFORM N-CAM 120).
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=89305258; PubMed=3253057;
 RA Barton C.H., Dickson G., Gower H.J., Rowett L.H., Putt W., Elsom V., Moore S.E., Gortidis C., Walsh F.S.;
 RT "Complete sequence and in vitro expression of a tissue-specific phosphatidylinositol-linked N-CAM isoform from skeletal muscle";
 RL Development 104:165-173(1988).
 RN 12
 RP SEQUENCE OF 491-761 FROM N.A. (ISOFORM N-CAM 120).

RC TISSUE=Skeletal muscle;
 RX MEDLINE=87301755; PubMed=2887295;
 RA Dickson G., Gower H.J., Barton C.H., Prentice H.M., Elsom V.L., Moore S.E., Cox R.D., Quinn C., Putt W., Walsh F.S.;
 RT "Human muscle neural cell adhesion molecule (N-CAM): identification of a muscle-specific sequence in the extracellular domain";
 RL Cell 50:1119-1130(1987).
 RN 13
 RP SEQUENCE OF 491-655 FROM N.A. (ISOFORM C).
 RX MEDLINE=89077552; PubMed=3203385;
 RA Gower H.J., Barton C.H., Elsom V.L., Thompson V., Moore S.E., Dickson G., Walsh F.S.;
 RT "Alternative splicing generates a secreted form of N-CAM in muscle and brain";
 RL Cell 55:955-964(1988).
 CC -1- FUNCTION: This protein is a cell adhesion molecule involved in neuron-neuron adhesion, neurite fasciculation, outgrowth of neurites, etc.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=N-CAM 120;
 CC IsoId=P13592-2; Sequence=Displayed;
 CC Name=N-CAM 140;
 CC IsoId=P13591-1; Sequence=External;
 CC Name=C; Synonyms=Secreted;
 CC IsoId=P13592-1; Sequence=VSP 002587;
 CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC DATABASE: NAME=PROV; NOTE=CD guide CD56 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd56.htm".
 CC -----
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 CC -----
 CC EMBL: X16841; CAA34739.1; -
 CC EMBL: M17409; AAA59912.1; -
 CC EMBL: M22094; AAA59910.1; -
 CC EMBL: M22092; AAA59911.1; -
 CC EMBL: M22091; AAA59911.1; JOINED.
 CC PIR: A31635; A31635.
 CC PIR: S07784; IOHUNG.
 CC GeneW: HGNC:7656; NCAM1.
 CC MIM: 116930; -
 CC GO: GO:0016021; C:integral to membrane; TAS.
 CC GO: GO:0005886; C:plasma membrane; TAS.
 CC InterPro: IPR008957; FN_III-like.
 CC InterPro: IPR003961; FN_III.
 CC InterPro: IPR007110; Ig-like.
 CC InterPro: IPR003598; Ig_c2.
 CC Pfam: PF00041; fn3; 2.
 CC Pfam: PF00047; Ig; 5.
 CC SMART: SM00060; FN3; 2.
 CC SMART: SM00408; IGC2; 5.
 CC PROSITE: PS50835; Ig_Like; 5.
 KW Immunoglobulin domain; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW GPI-anchor; Alternative splicing.
 FT SIGNAL 1 19
 FT CHAIN 20 761
 FT DOMAIN 20 111
 FT DOMAIN 116 205
 FT DOMAIN 212 301
 FT DOMAIN 308 406
 FT DOMAIN 406 491
 FT DOMAIN 518 595
 FT DOMAIN 660 727
 FT DISULFID 41 96
 NEURAL CELL ADHESION MOLECULE 1, 120 kDa
 ISOFORM.
 IG-LIKE C2-TYPE 1.
 IG-LIKE C2-TYPE 2.
 IG-LIKE C2-TYPE 3.
 IG-LIKE C2-TYPE 4.
 IG-LIKE C2-TYPE 5.
 FIBRONECTIN TYPE-III 1.
 FIBRONECTIN TYPE-III 2.
 PROBABLE.


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FT CONFLICT 239 239 G -> R (IN REF. 2).
FT CONFLICT 490 490 L -> F (IN REF. 2).
FT CONFLICT 599 600 OG -> F (IN REF. 3).
FT CONFLICT 720 721 MISSING (IN REF. 3).
FT CONFLICT 811 811 G -> A (IN REF. 3).
SQ SEQUENCE 848 AA, 93360 MW, 6802F0C0E6C1C2AD CRC64;

Query Match 8.6%; Score 135; DB 1; Length 848;
Best Local Similarity 23.2%; Pred. No. 0.0059;
Matches 64; Conservative 49; Mismatches 11; Indels 52; Gaps 13;

QY 63 SITVTVAAGNIGEDGILSCF-----EPDIKSLDIYQWKEGVLVHEFKGDE 116
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 77 SSSLTITVNA-NIDDAIGIKCVATGEGSESEATVAVKIFQKLMFNAPTPQEFREGDA 135
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 LSGODEM-----FRGRATVAFADQY---IVGNASLRKKNVQLTDGATKCYITTSK 163
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 136 VIVCDVVSLLPPTITMKHKGVDYLKKDVFVLSNNYIQIKGKTKDGTGYRC-----E 190
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 164 G-----KGNANLEKYGAFGMPB-----VNVDVN-ASSETLRCEAPWFQPTVVMAS 210
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 191 GRIARGEINFDIQIVAVVPTIQARQNIIVATNLGGSVILVCDN-BGFPEPTMSWK 249
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QY 211 QVDQGANSEVNTSEFELSENVTMKVSVLVNVTINNTYSCMIENDIAK--ATGDIKYT 268
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DB 306 AKPKITYVENQJAMELEQVITLCEASGDPISITW 341

RESULT 15
SHS1_HUMAN STANDARD: PRT: 503 AA
ID SHS1_HUMAN Q00683; Q63799; Q8N517; Q8TA8; Q9H022; Q9UDX2; Q9UIU6;
AC Q9YU09;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Protein-tyrosine phosphatase non-receptor type substrate 1 precursor
DE (SHP substrate-1) (SHPs-1) (Inhibitory receptor SHS-1) (Signal-
DE regulatory protein alpha-1) (SIRP-alpha-1) (SIRP-alpha-2) (SIRP-alpha-
DE 3) (MYD-1 antigen) (Brain Ig-like molecule with tyrosine-based
DE activation motifs) (Blt) (Macrophage fusion receptor) (p84).
GN PTPNS1 OR SHPS1 OR SIRP OR MYD1 OR BIR OR MFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=97223399; PubMed=9070220;
RA Yamao T., Matczak T., Amano K., Matsuda Y., Takahashi N., Ochi F.,
RA Fujioka Y., Kasuga M.;
RT "Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal
RT localization of genes.";
RL Biochem. Biophys. Res. Commun. 231:61-67(1997).
RN (2)
RP SEQUENCE FROM N.A. (ISOFORM 1). POLYMORPHISM, PHOSPHORYLATION,
RP N-GLYCOSYLATION, AND INTERACTIONS WITH PTPN11, PTPN6 AND GRB2.
RC TISSUE=placenta;
RX MEDLINE=97215901; PubMed=9062191;
RA Kharitonkov A., Chen Z., Sures I., Wang H., Schilling J.,
RA Ulich A.;
RT "A family of proteins that inhibit signalling through tyrosine kinase
RT receptors.";
RL Nature 386:181-186(1997).
RN (3)
RP SEQUENCE FROM N.A. (ISOFORM 3), AND VARIANTS ASP-95; LEU-96; ASN-100;
RP ARG-107; GLY-109 AND VAL-131.
RC TISSUE=monocytes;

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RX MEDLINE=98143722; PubMed=9485180;
RA Brooke G.P., Parsons K.R., Howard C.J.;
RT "Cloning of two members of the SIRP alpha family of protein tyrosine
RT phosphatase binding proteins in cattle that are expressed on monocytes
RT and a subpopulation of dendritic cells and which mediate binding to
RT CD4 T cells.";
RL Eur. J. Immunol. 28:1-11(1998).
RN (4)
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-44; THR-50; THR-52;
RP ARG-54; ALA-57; GLY-75; ASP-95; LEU-96; ASN-100; ARG-107; GLY-109 AND
RP VAL-131.
RC TISSUE=Brain;
RX MEDLINE=20053880; PubMed=10585953;
RA Sano S.-I., Onishi H., Kubota M.;
RT "Gene structure of mouse BIR/SHPS-1.";
RL Biochem. J. 344:667-675(1999).
RN (5)
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida U.P., Babbage A.K., Begguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corry N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahnam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Latyd G.K., Lawlor S.,
RA Levasalho M.H., Levertha M.A., Lloyd C., Lloyd D.M., McMuray A.A.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLeay K., McMuray A.A.,
RA Milne S.A., Misty D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis U.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilmshurst L., Way P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN (6)
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS LEU-44; THR-50;
RP THR-52; ARG-54; ALA-57; GLY-75; ASP-95; LEU-96; ASN-100; ARG-107;
RP GLY-109 AND VAL-131.
RC TISSUE=Brain, Kidney, and Skin;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalins D.B.,
RA Schercher A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (7)

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OM protein - protein search, using sw model

Run on: May 11, 2004, 16:23:01 / Search time 47 Seconds
(without alignments)
1824.854 Million cell updates/sec

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Gapop 10.0 , Gapept 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1574	100.0	309	US-09-910-689-209	Sequence 209, Appx
3	1574	100.0	309	US-09-884-441-392	Sequence 392, App
4	1574	100.0	309	US-09-907-969-392	Sequence 392, App
5	1574	100.0	309	US-09-827-271-392	Sequence 392, App
6	1574	100.0	309	US-10-010-742-209	Sequence 209, App
7	1574	100.0	309	US-10-198-053-392	Sequence 392, App
8	1431	90.9	282	US-09-778-320-208	Sequence 208, App
9	1431	90.9	282	US-09-850-178-33	Sequence 33, App1
10	1431	90.9	282	US-09-877-065-8	Sequence 8, App1
11	1431	90.9	282	US-09-989-722-291	Sequence 291, App
12	1431	90.9	282	US-09-989-723-291	Sequence 291, App
13	1431	90.9	282	US-09-989-729-291	Sequence 291, App
14	1431	90.9	282	US-09-989-727-291	Sequence 291, App
15	1431	90.9	282	US-09-910-689-208	Sequence 208, App

16	1431	90.9	282	US-09-989-731-291	Sequence 291, App
17	1431	90.9	282	US-09-884-441-393	Sequence 393, App
18	1431	90.9	282	US-09-989-732-291	Sequence 291, App
19	1431	90.9	282	US-09-991-073-291	Sequence 291, App
20	1431	90.9	282	US-09-990-442-291	Sequence 291, App
21	1431	90.9	282	US-09-991-163-291	Sequence 291, App
22	1431	90.9	282	US-09-993-604-291	Sequence 291, App
23	1431	90.9	282	US-09-990-456-291	Sequence 291, App
24	1431	90.9	282	US-09-989-421-291	Sequence 291, App
25	1431	90.9	282	US-09-992-598-291	Sequence 291, App
26	1431	90.9	282	US-09-896-738-2	Sequence 2, App1
27	1431	90.9	282	US-09-915-789A-5	Sequence 5, App1
28	1431	90.9	282	US-09-989-293A-291	Sequence 291, App
29	1431	90.9	282	US-09-989-735-291	Sequence 291, App
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43	1431	90.9	282	US-09-989-726-291	Sequence 291, App
44	1431	90.9	282	US-09-998-156-291	Sequence 291, App
45	1431	90.9	282	US-09-990-437-291	Sequence 291, App

ALIGNMENTS

RESULT 1
US-09-778-320-209
Sequence 209, Application US/09778320
Patent No. US20010034052A1
GENERAL INFORMATION:
APPLICANT: Dillion, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yugu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C5
CURRENT APPLICATION NUMBER: US/09/778.320
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 301
SOFTWARE: FaStSeq for Windows Version 3.0
SEQ ID NO 209
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-778-320-209

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Best Local Similarity 100.0%; Pred. No. 6.5e-138;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2 US-09-910-689-209

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; Sequence 209, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tonglong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910,689
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 209
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-689-209

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Best Local Similarity 100.0%; Pred. No. 6.5e-138;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3 US-09-884-441-392

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; Sequence 392, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; NUMBER OF SEQ ID NOS: 489
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US-09-884-441-392

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RESULT 4 US-09-907-969-392

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; Sequence 392, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Flinn, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Hall, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/09/907,969
; NUMBER OF SEQ ID NOS: 596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 392
; LENGTH: 309
; TYPE: PRT

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ORGANISM: Homo sapiens
US-09-827-271-392

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US-09-827-271-392
Sequence 392, Application US/09827271
Publication No. US20030165504A1
GENERAL INFORMATION:
APPLICANT: Recter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C6
CURRENT APPLICATION NUMBER: US/09/827, 271
CURRENT FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 461
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 392
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-827-271-392

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DB 1 HASAHASGROROLHSASTOIRMEPSPMASIGQLFWSISIIIIIIAGAILIIGFISG 60
QY 61 RHSITVTTVASAGNIGEDGILCTFEEDIKLSDIVIOWLKEGVLGVHEFEKGDLSQ 120
DB 61 RHSITVTTVASAGNIGEDGILCTFEEDIKLSDIVIOWLKEGVLGVHEFEKGDLSQ 120
QY 121 DEMFRGTAVFADQVIVGNASRLKXVQLTDAGTYKCYIITSGKGNANLEYKTGA 180
DB 121 DEMFRGTAVFADQVIVGNASRLKXVQLTDAGTYKCYIITSGKGNANLEYKTGA 180
QY 181 EVAVDVYASSETLRCEAPRFPPTVVMASQVDGANSFSEVNTSFEINSENYTMKV 240
DB 181 EVAVDVYASSETLRCEAPRFPPTVVMASQVDGANSFSEVNTSFEINSENYTMKV 240
QY 241 LYNVTINNTYSCMIENDIAKATGDIKVTSEIKRSHLQILNSKASLCVSSFFAIS 300
DB 241 LYNVTINNTYSCMIENDIAKATGDIKVTSEIKRSHLQILNSKASLCVSSFFAIS 300

DB 241 LYNVTINNTYSCMIENDIAKATGDIKVTSEIKRSHLQILNSKASLCVSSFFAIS 300
QY 301 PLSPLYMLK 309
DB 301 PLSPLYMLK 309

RESULT 6

US-10-010-742-209
Sequence 209, Application US/10010742
Publication No. US20020146727A1
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yugu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Wang, Tongrong
APPLICANT: McNeill, Patricia D.
APPLICANT: Harlocker, Susan L.
APPLICANT: Bennington, Angela Ann
APPLICANT: Zehentner, Barbara
APPLICANT: Fanger, Gary R.
APPLICANT: Recter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C7
CURRENT APPLICATION NUMBER: US/10/010, 742
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 307
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 209
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-10-010-742-209

Query Match 100.0%; Score 1574; DB 13; Length 309;
Best Local Similarity 100.0%; Pred. No. 6.5e-138;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAHASGROROLHSASTOIRMEPSPMASIGQLFWSISIIIIIIAGAILIIGFISG 60
DB 1 HASAHASGROROLHSASTOIRMEPSPMASIGQLFWSISIIIIIIAGAILIIGFISG 60
QY 61 RHSITVTTVASAGNIGEDGILCTFEEDIKLSDIVIOWLKEGVLGVHEFEKGDLSQ 120
DB 61 RHSITVTTVASAGNIGEDGILCTFEEDIKLSDIVIOWLKEGVLGVHEFEKGDLSQ 120
QY 121 DEMFRGTAVFADQVIVGNASRLKXVQLTDAGTYKCYIITSGKGNANLEYKTGA 180
DB 121 DEMFRGTAVFADQVIVGNASRLKXVQLTDAGTYKCYIITSGKGNANLEYKTGA 180
QY 181 EVAVDVYASSETLRCEAPRFPPTVVMASQVDGANSFSEVNTSFEINSENYTMKV 240
DB 181 EVAVDVYASSETLRCEAPRFPPTVVMASQVDGANSFSEVNTSFEINSENYTMKV 240
QY 241 LYNVTINNTYSCMIENDIAKATGDIKVTSEIKRSHLQILNSKASLCVSSFFAIS 300
DB 241 LYNVTINNTYSCMIENDIAKATGDIKVTSEIKRSHLQILNSKASLCVSSFFAIS 300
QY 301 PLSPLYMLK 309
DB 301 PLSPLYMLK 309

RESULT 7

US-10-198-053-392
Sequence 392, Application US/10198053
Publication No. US20030124140A1
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Retter, Marc W.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Hill, Paul
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.462C9
 ; CURRENT APPLICATION NUMBER: US/10/198.053
 ; CURRENT FILING DATE: 2002-07-17
 ; NUMBER OF SEQ ID NOS: 624
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 392
 ; LENGTH: 309
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-198-053-392

Query Match 100.0%; Score 1574; DB 14; Length 309;
 Best Local Similarity 100.0%; Pred. No. 6,5e-138;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAHASGRORLHASTOIRMEPSPAVASIGQILFMSIIIIIIAGATLIIIGFISG 60
 DB 1 HASAHASGRORLHASTOIRMEPSPAVASIGQILFMSIIIIIIAGATLIIIGFISG 60
 QY 61 RHSTVTTVASAGNIGEDGILSCTFEEDIKLSIDIVIQWLKGVGLVHEFEKGDSEQ 120
 DB 61 RHSTVTTVASAGNIGEDGILSCTFEEDIKLSIDIVIQWLKGVGLVHEFEKGDSEQ 120
 QY 121 DEMRGRRAVADQIVYANALRLKNOVLTAGTYKCYIITSKKGANLEFKTGAFSMP 180
 DB 121 DEMRGRRAVADQIVYANALRLKNOVLTAGTYKCYIITSKKGANLEFKTGAFSMP 180
 QY 121 DEMRGRRAVADQIVYANALRLKNOVLTAGTYKCYIITSKKGANLEFKTGAFSMP 180
 DB 121 DEMRGRRAVADQIVYANALRLKNOVLTAGTYKCYIITSKKGANLEFKTGAFSMP 180
 QY 181 EVNDVYASSETLCEAPRFPPTVWASOVDOGANFSEVNTSFEINSENVTKVSV 240
 DB 181 EVNDVYASSETLCEAPRFPPTVWASOVDOGANFSEVNTSFEINSENVTKVSV 240
 QY 241 LYNTVNTYSCMIENDIAKATGDIKYTESEIKRSHQLNSXASLCVSSFFAISWALL 300
 DB 241 LYNTVNTYSCMIENDIAKATGDIKYTESEIKRSHQLNSXASLCVSSFFAISWALL 300
 QY 301 PLSPLYMLK 309
 DB 301 PLSPLYMLK 309

RESULT 8
 ; US-09-778-320-208
 ; Sequence 208, Application US/09778320
 ; Patent No. US20010034052A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Mitcham, Jennifer
 ; APPLICANT: Wang, TongTong
 ; APPLICANT: McNeill, Patricia D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.491C5
 ; CURRENT APPLICATION NUMBER: US/09/778.320
 ; CURRENT FILING DATE: 2001-02-06
 ; NUMBER OF SEQ ID NOS: 301
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 208
 ; LENGTH: 282
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-778-320-208

Query Match 90.9%; Score 1431; DB 9; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1.1e-124;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASIGQILFMSIIIIIIAGATLIIIGFISGRHSITVTT
 DB 1 MASIGQILFMSIIIIIIAGATLIIIGFISGRHSITVTT
 QY 88 DIKLSDIVIQWLKGVGLVHEFEKGDSEODEMRGRTA
 DB 61 DIKLSDIVIQWLKGVGLVHEFEKGDSEODEMRGRTA
 QY 148 QLTDACTYKCYIITSKKGANLEFKTGAFSMPENVYANASSE
 DB 121 QLTDACTYKCYIITSKKGANLEFKTGAFSMPENVYANASSE
 QY 208 WASOVDOGANFSEVNTSFEINSENVTKVSVLYNTVNTYSCMIENDIAKATGDIK 267
 DB 181 WASOVDOGANFSEVNTSFEINSENVTKVSVLYNTVNTYSCMIENDIAKATGDIK 240
 QY 268 TSEIKRSHQLNSXASLCVSSFFAISWALLPLSPYMLK 309
 DB 241 TSEIKRSHQLNSXASLCVSSFFAISWALLPLSPYMLK 282

RESULT 9
 ; US-09-850-178-33
 ; Sequence 33, Application US/09850178
 ; Patent No. US20020034749A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Billing-Medel, Patricia A.
 ; APPLICANT: Cohen, Maurice
 ; APPLICANT: Colipite, Tracey L.
 ; APPLICANT: Friedman, Paula N.
 ; APPLICANT: Russell, John C.
 ; APPLICANT: Granados, Edward N.
 ; APPLICANT: Hodges, Steven C.
 ; APPLICANT: Klaes, Michael R.
 ; APPLICANT: Kratochvil, Jon D.
 ; APPLICANT: Roberts-Rapp, Lisa
 ; APPLICANT: Stroupe, Stephen D.
 ; APPLICANT: Gordon, Julian
 ; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
 ; FILE REFERENCE: 6251.US.P1
 ; CURRENT APPLICATION NUMBER: US/09/850.178
 ; CURRENT FILING DATE: 2001-05-07
 ; PRIOR APPLICATION NUMBER: US 08/972.376
 ; PRIOR FILING DATE: 1997-11-18
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 33
 ; LENGTH: 282
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-850-178-33

Query Match 90.9%; Score 1431; DB 9; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1.1e-124;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASIGQILFMSIIIIIIAGATLIIIGFISGRHSITVTTASAGNIGEDGILSCTFE 87
 DB 1 MASIGQILFMSIIIIIIAGATLIIIGFISGRHSITVTTASAGNIGEDGILSCTFE 60
 QY 88 DIKLSDIVIQWLKGVGLVHEFEKGDSEODEMRGRTAVADQIVYANASLRLKV 147
 DB 61 DIKLSDIVIQWLKGVGLVHEFEKGDSEODEMRGRTAVADQIVYANASLRLKV 120
 QY 148 QLTDACTYKCYIITSKKGANLEFKTGAFSMPENVYANASSETLCEAPRFPPTV 207
 DB 121 QLTDACTYKCYIITSKKGANLEFKTGAFSMPENVYANASSETLCEAPRFPPTV 180
 QY 208 WASOVDOGANFSEVNTSFEINSENVTKVSVLYNTVNTYSCMIENDIAKATGDIK 267

Db 181 WASQVDQGANFSEVNSTSEFELNSENVTMKVSVLYNVTINNTYSQMIENDIAKATGDIKV 240
QY 268 TSEIKRSHLOLNSKASLCVSSFFAISMALLPISPYIMLK 309
Db 241 TSEIKRSHLOLNSKASLCVSSFFAISMALLPISPYIMLK 282

RESULT 10
US-09-877-065-8
Sequence 8, Application US/09877065
Patent No. US2002005190A1
GENERAL INFORMATION:
APPLICANT: OPLE, ERIC
APPLICANT: MCLACHLAN, KAREN
APPLICANT: HEARD, CHERYL J.
TITLE OF INVENTION: NOVEL GENE TARGETS AND LIGANDS THAT BIND THERETO FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF OVARIAN CARCINOMAS
FILE REFERENCE: 037003-0280631
CURRENT APPLICATION NUMBER: US/09/877,065
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210,451
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 282
TYPE: PRT
ORGANISM: Homo sapiens
US-09-877-065-8

Query Match 90.9%; Score 1431; DB 9; Length 282;
Best Local Similarity 100.0%; Pred. No. 1,1e-124; Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGILFMSIISIIIIAGAIALIGISGRHSITVTYASAGNIGEDGILSTCEP 87
Db 1 MASLGILFMSIISIIIIAGAIALIGISGRHSITVTYASAGNIGEDGILSTCEP 60
QY 88 DIKLSDIVIOMLKEGVGLVHEFKKSGDELSDODEFRGRTVFPDQVIVGNASRLKNV 147
Db 61 DIKLSDIVIOMLKEGVGLVHEFKKSGDELSDODEFRGRTVFPDQVIVGNASRLKNV 120
QY 148 QLTDAATYKCYIITTSKGNANLKYTGAFSMEPVNVVDNASETLRCEAPRFPQPTVV 207
Db 121 QLTDAATYKCYIITTSKGNANLKYTGAFSMEPVNVVDNASETLRCEAPRFPQPTVV 180
QY 208 WASQVDQGANFSEVNSTSEFELNSENVTMKVSVLYNVTINNTYSQMIENDIAKATGDIKV 267
Db 181 WASQVDQGANFSEVNSTSEFELNSENVTMKVSVLYNVTINNTYSQMIENDIAKATGDIKV 240
QY 268 TSEIKRSHLOLNSKASLCVSSFFAISMALLPISPYIMLK 309
Db 241 TSEIKRSHLOLNSKASLCVSSFFAISMALLPISPYIMLK 282

RESULT 11
US-09-989-722-291
Sequence 291, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738

PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090682
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090683
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 90.9%; Score 1431; DB 9; Length 282;
Best Local Similarity 100.0%; Pred. No. 1, 1e-124;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGILFMSIIIIIIIIAGAILIIGISGRHSITVTVASAGNIGEDGILCTFEP 87
DB 1 MASLGILFMSIIIIIIIIAGAILIIGISGRHSITVTVASAGNIGEDGILCTFEP 60
QY 88 DIKLSDIVIOWLKEGVLGVHEFEKGGKDELSEODEMFRGRTAVFADQVIVGNASLRLKV 147
DB 61 DIKLSDIVIOWLKEGVLGVHEFEKGGKDELSEODEMFRGRTAVFADQVIVGNASLRLKV 120
QY 148 QLTDACTVCYIITSGKGNANLEKYTGAFSMEPVNDVNASSETLRCEAPRFPQPTVV 207
DB 121 QLTDACTVCYIITSGKGNANLEKYTGAFSMEPVNDVNASSETLRCEAPRFPQPTVV 180
QY 208 WASOVQGANFSEVSTSELSNENVTWVSVLVNNTNNYSCMIENDIAKATDIDY 267
DB 181 WASOVQGANFSEVSTSELSNENVTWVSVLVNNTNNYSCMIENDIAKATDIDY 240
QY 268 TSEIIRSRSHLQILNSKASLVCVSPFAISWALLPLSPYIMLK 309
DB 241 TSEIIRSRSHLQILNSKASLVCVSPFAISWALLPLSPYIMLK 282

RESULT 12
US-09-989-723-291
Sequence 291, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowald, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C62
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 90.9%; Score 1431; DB 9; Length 282;
Best Local Similarity 100.0%; Pred. No. 1,1e-124; Indels 0; Gaps 0;

Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MASIGQLIFMSIIIIIIIIAGAILIIGFGISGRHSITVTVAASNGIGEDGILSCFEP 60
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DB 61 DIKLSDIVIOMLKEGVGLVHEFEKGEKDEISEODEMFRGRTAVPADQVIYGNASIRLKNV 120
QY 148 QLTADAGYKCYIIISKKKGNANLEKYGAFSMPFVNVDYASSETLACEAPRPFQPTVV 207
DB 121 QLTADAGYKCYIIISKKKGNANLEKYGAFSMPFVNVDYASSETLACEAPRPFQPTVV 180
QY 208 WASQVDOGAFNSEVSNISFELNSENVTKVSVLYNNTYSCMIENDIAKATGDIKV 267
DB 181 WASQVDOGAFNSEVSNISFELNSENVTKVSVLYNNTYSCMIENDIAKATGDIKV 240
QY 268 TSEIKRRSHIQLINSAASLCSVSSFPFASWALLPLSYLMK 309
DB 241 TSEIKRRSHIQLINSAASLCSVSSFPFASWALLPLSYLMK 282

RESULT 13
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; Sequence 291, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Denoyers, Luc
; APPLICANT: Batou, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guirney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Demin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 90.9% Score 1431; DB 9; Length 282;
Best Local Similarity 100.0%; Pred. No. 1,1e-124; Indels 0; Gaps 0;
Matches 282; Conservative 0; Mismatches 0;

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QY 148 QLTDAGYTKCYIITSKGNANLLEKYGAFSWEVNVVYNASSETLRCEAPRPFQPTV 207
DB 121 QLTDAGYTKCYIITSKGNANLLEKYGAFSWEVNVVYNASSETLRCEAPRPFQPTV 180

OY 208 WASOVDGANTSEVNTSIFELNSENVTMKVSVLYNTVNTTNTYSOMIENDIAKATGDIKV 267
DB 181 WASOVDGANTSEVNTSIFELNSENVTMKVSVLYNTVNTTNTYSOMIENDIAKATGDIKV 240
OY 268 TSEIKRSHLOLNKSKSLCVSSFFALSMALLPLSPITLMK 309
DB 241 TSEIKRSHLOLNKSKSLCVSSFFALSMALLPLSPITLMK 282

RESULT 14
US-09-989-727-291
Sequence 291, Application US/09989727
Patent No. US20020072497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bostein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1G65
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Query Match

Best Local Similarity 90.9%; Score 1431; DB 9; Length 282;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASIGQILFWSIIISIIIIAGALALIIFGISGRHSITVTVASAGNIGEDGIIISCTPEP 87
DB 1 MASIGQILFWSIIISIIIIAGALALIIFGISGRHSITVTVASAGNIGEDGIIISCTPEP 60

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QY 88 DIKLSIDIYIOMLKEGVILGVHEFEKGEKDELSEODEMERGRTRAVADQYIVGNASIRLKNV 147
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QY 148 QLTADGTYKCYIITSKGGNNANLEKYGAFSPMEVNVYNASSSETLRCEAPRPFQPTVV 207
DB 121 QLTADGTYKCYIITSKGGNNANLEKYGAFSPMEVNVYNASSSETLRCEAPRPFQPTVV 180
QY 208 WASQVDQGANFSEVSNISFELNSENVTMKVSVLYNTINNTYSCMIENDIAKATGDIKV 267
DB 181 WASQVDQGANFSEVSNISFELNSENVTMKVSVLYNTINNTYSCMIENDIAKATGDIKV 240
QY 268 TESIKRSHIQLNKSASLVCVSSFFAISMALLPLSPYIMLK 309
DB 241 TESIKRSHIQLNKSASLVCVSSFFAISMALLPLSPYIMLK 282

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RESULT 15

US-09-910-689-208

; Sequence 208; Application US/09910689
; Patent No. US20020081609A1

; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.

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; APPLICANT: Mitcham, Jennifer

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; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.491C6

; CURRENT APPLICATION NUMBER: US/09/910.689

; NUMBER OF SEQ ID NOS: 307

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 208

; LENGTH: 282

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-910-689-208

Query Match

Best Local Similarity 90.9%; Score 1431; DB 9; Length 282;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 DIKLSIDIYIOMLKEGVILGVHEFEKGEKDELSEODEMERGRTRAVADQYIVGNASIRLKNV 120
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DB 241 TESIKRSHIQLNKSASLVCVSSFFAISMALLPLSPYIMLK 282

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